

## **FIGURE 1**

ACTGCACCTCGGTTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA  
CCCACCGCGTCCGGGCCGGAGCAGCACGCCGCAGGACCTGGAGCTCCGGCTCGTCTCCCG  
CAGCGCTACCCGCCATCGCCTGCCGCCGGGGCGCTGGGCTCCTGCCGCTTGCTG  
CTGCTGCCGCCGCCGGAGGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGCT  
GGTGGACAAGTTAACCAAGGGATGGTGGACACCGCAAAGAAAGAACTTGGCGCGGGAAACA  
CGGCTTGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCCTGCTGGAGATC  
CTGGAGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA  
GCACCTGGAGGCCTGGTGGCTCAGCTGAAGAGCGAATATCCTGACTTATTGAGTGGTTT  
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCAGTGTCTCGCATGC  
CAGGGCGGATCCCAGAGGCCCTGCAGCGGAATGGCCACTGCAGCGAGATGGAGCAGACA  
GGCGACGGGTCTGCCGGTGCACATGGGTACCAGGGCCGCTGTGACTGACTGCATGG  
ACGGCTACTTCAGCTCGCTCCGAACGAGACCCACAGCATTGACAGCCTGTGACGAGTCC  
TGCAAGACGTGCTCGGCCCTGACCAACAGAGACTGCCGGAGTGTGAAGTGGCTGGGTGCT  
GGACGAGGGCGCTGTGGATGTGGACGAGTGTGCCGGAGCCGCTCCCTGCAGCGCTG  
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTG  
GGCTGCACAGGGAAAGGCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACGCAGGGAGCA  
CGGACAGTGTGCAGATGTGGACGAGTGCCTACTAGCAGAAAAACCTGTGTGAGGAAAAACG  
AAAATGCTACAATACTCCAGGGAGCTACGTCTGTGTGTCCTGACGGCTTCGAAGAAACG  
GAAGATGCCGTGTGCCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCGACACAGCT  
GCCCTCCCGCAAGACCTGTAATGTGCCGGACTTACCCCTAAATTATTGAGGATGTCC  
CGTGGAAAATGTGGCCTGAGGATGCCGTCTGCAGTGGACAGCGGGAGAGGCTGC  
CTGCTCTCTAACGGTTGATTCTCATTTGCCCTAAACAGCTGCATTCTGGTTGTTCTTA  
AACAGACTTGTATATTTGATACAGTTCTTGTAAATAAAATTGACCATTGTAGGTAATCAGG  
AGGAAAAAAAGGGCGCCGCGACTCTAGAGTGCACCTGCAGAAGC  
TTGCCGCCATGGCCAACCTGTTATTGCAGCTATAATGGTTACAAATAAGCAATAGCA  
TCACAAATTCAAAATAAGCATTTCAGCTAGTTGTGGTTGTC  
ATCAATGTATCTTATCATGTCTGGATCGGGATTAATTCCGCGCAGCACCATGCCCTGAAAT  
AACCTCTGAAAGAGGAACCTGGTTAGGTACCTCTGAGGCGAAAGAACCGAGCTGTGGAATG  
TGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAGCAG  
ATCTCAATTAGTCAGCAACCCAGTTT

## **FIGURE 2**

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLLPLLLLPPAPEAAKKPTPCHRGRGLVDKFNQGMVDTAKKNFGGGNTAEEKTLSKYESSEIRL  
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLKVCCSPGTYGPDCLACQGGSQRPCSG  
NGHCSGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNETHSICTACDESCKTCSGLTNRDCGECEVGWLDE  
GACVDVDECAAEPPPCSAAQFCKNANGSYTCEECDSSCVGCTGEGPNCKECISGYAREHGQCADVDEC SLAEKT  
CVRKNENCYNTPGSYVCVCPDGFETEDACVPPAEEATEGESPTQLPSREDL

**Signal peptide:**

amino acids 1-24

**N-glycosylation sites.**

amino acids 190-194 and 251-255

**Glycosaminoglycan attachment sites.**

amino acids 149-153 and 155-159

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 26-30

**Casein kinase II phosphorylation sites.**

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343  
and 349-353

**Tyrosine kinase phosphorylation site.**

amino acids 303-310

**N-myristoylation sites.**

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and  
313-319

**Aspartic acid and asparagine hydroxylation site.**

amino acids 308-320

**EGF-like domain cysteine pattern signature.**

amino acids 166-178

**Leucine zipper pattern.**

amino acids 94-116

## **FIGURE 3**

CAGGTCCAAC TGCACCTCGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTC  
GACCTCGACCCACGCGTCCGCCAGGCCGGAGGCAGCGCCAGCGTCAAACGGGAACA  
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGGCCAGGTTGCGTAGGTGCG  
GCACGAGGAGTTCCCGCAGCGAGGAGGTCTGAGCAGC **ATGGCCGGAGGAGCGCCTTC**  
**CCTGCCGCCGCTCTGGCTCTGGAGCATCCTCCTGTGCTGCTGGCACTGCGGCCAGGC**  
CGGGCCGCCAGGAGGAGGCCTGTACCTATGGATCGATGCTCACCAAGGAAAGAGTACTCA  
TAGGATTGAAGAAGATACTTGATTGTTCAGAGGGAAAATGGCACCTTACACATGAT  
TTCAGAAAAGCGCAACAGAGAATGCCAGCTATTCTGTCAATATCATTCCATGAATTTCAC  
CTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGAATTCTGTCTTGCCTCCCTGGATA  
AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGAAACAGTGCTCACAGGCA  
TCAGTTGTTCAAGTTGGTTCCATGTCTTGGAAAACAGGATGGGGTGGCAGCATTGAAGT  
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCAAACACACTCAAATGCTATCT  
TCTTAAACATGTCAACAAGCTGAGTCCCAGGGTGCAGAACATGGAGGCTTTGTAAT  
GAAAGACGCATCTGCGAGTGTCTGATGGTTCCACGGACCTCACTGTGAGAAAGCCCTTG  
TACCCACGATGTATGAATGGTGGACTTGTGACTCCTGGTTCTGCATCTGCCACCTG  
GATTCTATGGAGTGAAC TGTGACAAGCAAACACTGCTCAACCACCTGCTTAATGGAGGGACC  
TGTTCTACCCGGAAAATGTATTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAG  
CAAATGCCACAACCTGCGAAATGGAGGTAAATGCATTGGTAAAGCAAATGTAAGTGT  
CCAAAGGTTACCAAGGGAGACCTCTGTTCAAAGCCTGTCTGAGCCTGGCTGGTGCACAT  
GGAACCTGCCATGAACCAACAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAA  
TAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGCGCCAGCTCAGGCAGC  
ACACGCCCTCACTTAAAAGGCCGAGGAGCGGCCAGGATCCACCTGAATCCAATTACATCTGG  
**TGA**ACTCCGACATCTGAAACGTTTAAGTTACACCAAGTTCATAGCCTTGTAAACCTTCA  
TGTGTTGAATGTTCAAATAATGTTCAATTACACTTAAGAATACTGCCCTGAATTTCATTAGCT  
TCATTATAAAATCACTGAGCTGATATTACTCTTCTTTAAGTTCTAAGTACGTCTGTAG  
CATGATGGTATAGATTCTTGTGTTCACTGAGCTGATTTGAGATTTTAAATGTCATTGA  
TCAGGTTAAAATTTCAGTGTAGTTGGCAGATATTTCAAAATTACAATGCAATTGTT  
GTCTGGGGCAGGGAACATCAGAAAGGTTAAATTGGGAAAAATGCGTAAGTCACAAGAAT  
TTGGATGGTCAGTTAATGTTGAAGTTACAGCATTTCAGATTATTGTCAGATATTAGAT  
GTTGTTACATTTTAAAATTGCTCTTAATTTCAAAATTCTCAATACAATATATTGACC  
TTACCAATTCCAGAGATTCACTGAGCTTAAATTTTAAATTACAATGCTGGTAGTGGCATT  
AAACAATATAATATCTAAACACAATGAAATAGGAATATAATGTATGAACCTTGCAT  
TGGCTTGAAGCAATATAATATTGTAACAAAACACAGCTCTTACCTAATAAACATTTAT  
ACTGTTGTATGTATAAAATAAAGGTGCTGCTTAGTTTTGGAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAGGGCGGCCGCACTCTAGAGTCGACCTGCAGAAGCTTGGC  
GCCATGGCCCAACTTGTATTGCAGCTTATAATG

## **FIGURE 4**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLWSILLCLLALRAEAGPPQEEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFSLRSLDKGIMADPTVNVPPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNNGFCNERRICECPDGFHGPHEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTFCYPGKCICPPGLEGEQCEISKCPQPCRNGGKCIKGSKCKCSKGYQGDLCSPVVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEERRDP
PESNYIW
```

**Signal peptide:**

amino acids 1-28

**N-glycosylation site.**

amino acids 88-92, 245-249

**Casein kinase II phosphorylation site.**

amino acids 319-323

**Tyrosine kinase phosphorylation site.**

amino acids 370-378

**N-myristoylation sites.**

amino acids 184-190, 185-191, 189-195, 315-321

**ATP/GTP-binding site motif A (P-loop).**

amino acids 285-293

**EGF-like domain cysteine pattern signature.**

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

## **FIGURE 5**

CGGACGCGTGGCGTCGGCGGTGCAGAGCCAGGAGGCCAGGAGGCCACC**ATGTGGCGATGTCCACTGGGGCTAC**  
TGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGGTGCCACGCAGGGCTGTGGCGCCGG  
GAGCTAGCACCGGGCTCGCACCTGCAGGGCATCCGGACGCCGGAGGCCGGTACTGCCAGGA  
GCAGGACCTGTGCTGCCGCGCGTGCAGCAGTGTGCCCTGCCACCTGGCGCCATCT  
GTTACTGTGACCTCTTGCAACCGCACGGCTCCGACTGCTGCCCTGACTTCTGGGACTTC  
TGCCTCGCGTGCCACCCCCCTTCCCCGATCCAAGGATGTATGCATGGAGGTGCTATCTA  
TCCAGTCTTGGAACGTACTGGACAACGTAAACCGTTGCACCTGCAGGAGAACAGGCAGT  
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG  
GAACACAGGCCCTCTGGGCATGACCCTGGATGAGGCATTGCTACGCCTGGCACCA  
TCCGCCCATCTCCTCGGTATGAACATGCATGAAATTATAACAGTGTGAAACCCAGGGAG  
GTGCTTCCCACAGCCTCGAGGCCTCTGAGAACGTGGCCAACCTGATTGATGAGCCTCTGA  
CCAAGGCAACTGTGCAGGCTCTGGCCTCTCCACAGCAGCTGTGCATCCGATGTGTCT  
CAATCCATTCTCTGGGACACATGACGCCGTGCTGTGCCCCAGAACCTGCTGTGAC  
ACCCACCAGCAGCAGGGCTGCCCGTGGCGTCTCGATGGTGCCTGGTGGTCCCTGCGTCG  
CCGAGGGGTGGTGTCTGACCACGTCTACCCCTCTCGGGCGTGAACGAGACGGAGCTGGCC  
CTGCCCCCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGCAAGGCCAGGCCACTGCC  
CACTGCCCAACAGCTATGTTAAACAAATGACATCTACCAAGTCACTCCTGTCTACCGCCT  
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAACGGCCCTGTCAAGCCCTCA  
TGGAGGTGCATGAGGACTTCTTCCATACAGGGAGGCATCTACAGCCACAGCCAGTGAGC  
CTTGGGAGGCCAGAGAGATACGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG  
AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCCAACCTGGGCC  
CAGCCTGGGGCGAGAGGGCCACTTCCGCATCGTGCAGCGTCAATGAGTGCAGCATCGAG  
AGCTCGTGTGGCGTCTGGGCGCTGGGCGTGGGATCCAGGCTAAGGGCGGGCGAAGAGGCCCAATG  
GGCGGTGACCCAGCCTGCCGACAGAGGCCGGCGCAGGCCGGCGCAGGGCGCTAAT  
CCCGCGCGGGTTCCGCTGACGCAGGCCCGCTGGGAGGCCGGCGAGGCGAGACTGGCG  
GAGCCCCAGACCTCCAGTGGGGACGGGGCAGGGCTGGGCTGGGAAGAGCACAGCTGCAG  
ATCCCAAGGCCCTGGGCCCTGGATCCAGGCTAAGGCTAACCTCAAGTCTCCAGC  
CCCAATAACCCACCCAAATCCGTATTCTTTTTTTAGACAGGGCTTGCTCCG  
TTGCCCAAGGTGGAGTGCAGTGGCCATCAGGGCTCACTGTAACCTCCGACTCTGGTTCA  
AGTGACCTCCACCTCAGCCTCTCAAGTAGCTGGACTACAGGTGCACCACACCTGGC  
TAATTTGTATTTGTAAAGAGGGGGTCTCACTGTGTTGCCAGGCTGGTTCGAACT  
CCTGGGCTCAAGCGGTCCACCTGCCCTCCCAAAGTGTGGATTGCAGGCATGAGCC  
ACTGCACCCAGCCCTGTATTCTTATTCTCAGATATTATTTCTTCACTGTTAAAAA  
TAAAACCAAGTATTGATAAAAAAAA

## **FIGURE 6**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLCCRGRAADD
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPPFPIQGCMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEQRLLGHDPG
```

**N-glycosylation site.**

amino acids 78-82, 161-165

**Casein kinase II phosphorylation site.**

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,  
411-415

**N-myristoylation site.**

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,  
269-275, 378-384, 442-448

**Amidation site.**

amino acids 26-30, 318-322

**Eukaryotic thiol (cysteine) proteases histidine active site.**

amino acids 398-409

## **FIGURE 7**

AGGCTCCTTGGCCCTTTCCACAGCAAGCTTNTGCNATCCCGATTGTTGTCTCAAATCCA  
ATTCTCTTGGGACACATNACGCCTGTCCTTNGCCCCAGAACCTGCTGTCTGTACACCCAC  
CAGCAGCAGGGCTGCCCGNTGGCGTCTCGATGGTGCCTGGTGGTCTGCGTCGCCGAGG  
GNTGGTGTCTGACCACTGCTACCCCTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC  
CCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGCAAGCGCCAGGCCACTGCCACTGC  
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTGGCTC  
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTATGGAGG  
TGCATGAGGACTTCTTCCATAAGGGAGGCATCTACAGCCACAGGCCAGTGAGCCTTGGG  
AGGCCAGAGAGATAACGCCGGCATGGACCCACTCAG

## **FIGURE 8**

GCTGCTTGCCTGTTGATGGCAGGCTTGCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT  
CCTGCAAAGCCCAGGTGAGCAACGAGGATGACTGCCCTGCAGGTGGAGAATGTCACCCAGCTGGGG  
GAGCAGTGCTGGACCCGCGCATCCGCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG  
CAGCTTGAACTGCGTGGATGACTCACAGGACTACTACGTGGCAAGAAGAACATCACGTGCT  
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGCCATCCTT  
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGACCCGCCAGCTATAGGCTCTGGGGGG  
CCCCGCTGCAGCCCACACTGGGTGTGGTCCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG  
GCCCAGTGGAGCCTGCCTGGTTCCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT  
CTGCACCCCTGTCCCCCACCCGTGACACAGATCCGCCTGCAGATGGCCCTCCAACCCCTCTGCTGTTTC  
CATGGCCCAGCATTCTCCACCCTTAACCCCTGTGCTCAGGCACCTCTCCCCCAGGAAGCCTT  
CCCTGCCACCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCCGACCCAGCA  
GGGGACAGGCACTCAGGAGGGCCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAAACTGGA  
GGACAAGAGTCGACGTGAGTTCCTGGAGTCTCCAGAGATGGGCCTGGAGGCCTGGAGGAA  
GGGGCCAGGCCTCACATTCGTGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT  
AATAAACACCTGTTGGATAAGCAAAAAAA

## **FIGURE 9**

MTHRTTWARRTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCSDPASYRLWGAPLQPT  
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHDPPMALSRTPTRQISSLDT  
DPPADGPSNPLCCCFHGPAFSTLNPVLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

**Signal peptide:**

amino acids 1-47

**N-glycosylation site.**

amino acids 31-35, 74-78, 84-88

**Casein kinase II phosphorylation site.**

amino acids 22-26, 76-80

**N-myristoylation site.**

amino acids 56-60

**Amidation site.**

amino acids 70-74

## **FIGURE 10**

CCCATCGCGTCCGAACCTCTCCAGCGATGGGAGCCGCCGCCTGCTGCCAACCTCACTCTGT  
GCTTACAGCTGCTGATTCTCTGCTGTCAAACACTCAGTACGTGAGGGACCAGGGCGCCATGACC  
GACCAGCTGAGCAGGCCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA  
CGTGCAGGTACCGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTGCCAAGC  
TCATAGTGGAGACGGACACGTTGGCAGCCGGGTTCGCATCAAAGGGCTGAGAGTGAGAAG  
TACATCTGTATGAACAAGAGGGCAAGCTCATGGGAAGCCCAGCGGGAAAGAGCAAAGACTG  
CGTGTTCACGGAGATCGTGGAGAACAACTATA CGGCCTTCCAGAACGCCGGCACGAGG  
GCTGGTTCATGGCCTTCACGCCGCAGGGCGGCCAGGCTTCCGCAGGCCAGAAC  
CAGCGCGAGGCCCACTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTCCCCAACCACGC  
CGAGAAGCAGAAGCAGTCGAGTTGGCTCCGCCCCACCCGCCGACCAAGGCCACAC  
GGCGGCCAGCCCTCACGTAGTCTGGGAGGCAGGGGCAGCAGGCCCTGGCCGCCTCCC  
CACCCCTTCCCTTAATCCAAGGACTGGCTGGGTGGCGGGAGGGAGGCCAGATCCCC  
GAGGGAGGACCCCTGAGGCCCGAAGCATCCGAGCCCCCAGCTGGGAAGGGCAGGCCGGTG  
CCCCAGGGCGGCTGGCACAGTGCCCTTCCGGACGGTGGCAGGCCCTGGAGAGGAAC  
GAGTGTCAACCTGATCTCAGGCCACCAGCCTCTGCCGCCCTCCAGCCGGCTCCTGAAGCC  
CGCTGAAAGGTCA CGCACTGAAGGCCTGCAGACAACCGTCTGGAGGTGGCTGTCCCTAAAA  
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCTCAGGCCCCAAACTCCTCCTGGCTAGACTGTA  
GGAAGGGACTTTGTTGTTGTTGTTCAAGGAAAAAAGAAAGGGAGAGAGAGGAAAATAG  
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCACCCCAACTCCCAGCCC  
CGGAATAAAACCATTTCCTGC

## **FIGURE 11**

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHKVQVTGRRI  
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLIGKPSGKSKDCVFTEIVLE  
NNYTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEF  
VGSAPTRRTKRTRRPQPLT

**Signal peptide:**

amino acids 1-22

**N-glycosylation site.**

amino acids 9-13, 126-130

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 60-64

**Casein kinase II phosphorylation site.**

amino acids 65-69

**Tyrosine kinase phosphorylation site.**

amino acids 39-48, 89-97

**N-myristoylation site.**

amino acids 69-75, 188-194

**Amidation site.**

amino acids 58-62

**HBGF/FGF family signature.**

amino acids 103-128

## FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAATTCTCCCTGTTGAATTTTCACATGGAG  
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTAC  
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCACAGAACCCATCCAGT  
CATTGATTGCTGTTATTCCCCCTTTCTTCCACCATTTGATTTAT  
TTCCGTACTTCAGAAATGGGCTACAGACCACAAAGTGGCCAGCCATGGGCTTTTCCT  
GAAGTCTTGGCTTATCATTCCCTGGGCCTACTCACAGGTGTCCAAACTCCTGGCCTGCC  
CTAGTGTGTGCCGCTGCGACAGGAACCTTGTCTACTGTAATGAGCGAAGCTGACCTCAGTG  
CCTCTGGGATCCCGAGGGCGTAACCGTACTCTACCTCCACAACAACCAAATTAATAATGC  
TGGATTCCTGCAGAACTGCACAATGTACAGTCGGTGACACGGTCTACCTGTATGGCAACC  
AACTGGACGAATTCCCCATGAACCTCCAAAGAATGTCAGAGTTCTCCATTGCAGGAAAAC  
AATATTAGACCATTCACGGGCTGCTTGTCCCAGCTTGAAGCTTGAAGAGCTGCACCT  
GGATGACAACCTCCATATCCACAGTGGGGTGGAAAGACGGGCCTCCGGGAGGCTATTAGCC  
TCAAATTGTTGTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTGGCTTCCTGTGGAC  
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTATATCCGACATGGCCTTCAGAA  
TCTCACGAGCTTGGAGCGTCTTATTGTGGACGGGAACCTCCTGACCAACAAGGGTATGCCG  
AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTCATAATTGTACGTAATTGCCGTGTC  
CACCCCTCCTCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGCAGGACAACCAAGAT  
AAACCACATTCTTGACAGCCTCTCAAATCTCGTAAGCTGGAAACGGCTGGATATATCCA  
ACAACCAACTGCGGATGCTGACTCAAGGGTTTGATAATCTCTCAAACCTGAAGCAGCTC  
ACTGCTCGGAATAACCCCTGGTTGTGACTGCAGTATTAAATGGGTACAGAATGGCTCAA  
ATATATCCCTCATCTCTCACAGTGCAGGGTTCATGTGCCAAGGTCTGAACAAGTCCGGG  
GGATGGCCGTAGGGAAATTAAATGAATCTTGCTCTGCCCACACGACCCCCGGCCTG  
CCTCTCTCACCCAGCCCCAAGTACAGCTCTCCGACCACCTCAGCCTCCCACCCCTCTAT  
TCCAAACCTAGCAGAAGCTACACGCCTCCAACCTCCTACCAACATCGAAACTTCCCACGATT  
CTGACTGGGATGGCAGAGAAAGAGTGACCCCACCTATTCTGAACGGATCCAGCTCTATC  
CATTGTTGATGACTTCCATTCAAGTCAGCTGGCTCTCTCTCACCCTGATGGCATA  
CAAACTCACATGGGTGAAATGGCCACAGTTAGTAGGGGCATCGTTAGGAGCGCATAG  
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT  
TGTTAGTGCCACTGGATGCTTTAACTACCGCGCGTAGAAGACACCAATTGTCAGAGGC  
CACCAACCATGCCTCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA  
CGTCCCACAGCATGGCTCCCCCTTCTGCTGGCGGGCTTGTATGGGGCGCGGTGATATTT  
GTGCTGGTGGCTTGCTCAGCGTCTTGTGGCATATGCACAAAAAGGGCGCTACACCTC  
CCAGAAGTGGAAATAACAACCGGGCGCGAAAGATGATTATGCGAGGCAGGCACCAAGA  
AGGACAACCTCCATCCTGGAGATGACAGAAACCGAGTTTCAGATCGTCTCCTTAATAACGAT  
CAACTCCTTAAAGGAGATTTCAGACTGCAGCCATTACACCCAAATGGGGCATTAATTA  
CACAGACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGC  
ACTGCCATACGTGAAGCCAGAGGCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAA  
CACACTCGTGTGTCACATAAAGACACGCAGATTACATTGATAATGTTACACAGATGCAT  
TTGTCATTTGAATACTCTGTAATTATACGGTGTACTATATAATGGGATTAAAAAGTG  
CTATCTTCTATTCAAGTTAATTACAAACAGTTGTAACCTTGCTTTAAATCTT

## **FIGURE 13**

MGLQTTKWPISHGAFFLKSWEIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP  
EGVTVLYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENNIQTI  
SRAALAQLLKLEELHLDNSISTVGVEDGAFREAIISLKLFLSKNHLSVPVGLPVDLQELR  
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKEFSIVRNSLSHPPPD  
LPGTHLIRYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLNSNLKQLTARNN  
PWFCDCSIKWVTEWLKYIPSSLNVRGFMCQGPEQVRGMAVRELNMNLLSCPTTPGLPLFTP  
APSTASPTTQPPTLSIPNPSRSYTPPTTSLPTIPDWGGRERVTPPISERIQLSIHFVND  
TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL  
DAFNYRAVEDTICSEATTHASYLNNGSNTASSHEQTSHSMGSPFLLAGLIGGAVIFVLVVL  
LSVFCWHMHKKGRYTSQWKYNRGRRKDYCEAGTKKDNSILEMTETSFQIVSLNNDQLLKG  
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

**Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 542-561

**N-glycosylation site.**

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

**Casein kinase II phosphorylation site.**

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

**Tyrosine kinase phosphorylation site.**

amino acids 319-328

**N-myristoylation site.**

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,  
522-528, 545-551, 633-639

**Amidation site.**

amino acids 581-585

**Leucine zipper pattern.**

amino acids 164-186

**Phospholipase A2 aspartic acid active site.**

amino acids 39-50

## **FIGURE 14**

ACTTGGAGCAAGCGGCGGCCGGAGACAGAGGCAGAGGCAGAACAGCTGGGCTCCGTCTCGCCTCCCACGAGCG  
ATCCCCGAGGAGAGCCGCGGCCCTCGCGAGGCCAAGAGGCCAGAGGAAGACCCGGGTGGCTCGGCCCTGCC  
TCGCTTCCCAGGCAGGCCGGCTGCAGCCTTGCCCTCTTGCTCGCCITGAAAATGGAAAAGATGCTCGCAGGCT  
GCTTCTGCTGATCCTCGGACAGATCGTCCTCCCTGCCAGGGAGGCCAGGGAGCGTCAGTGAGGAGGTTCCATCT  
CTAGGGCAGACACGCTCGGACCCACCGCAGACGGCCCTCTGGAGAGTTCCTGTGAGAACAAAGCAGGGCAGACC  
TGGTTTCATCATTGACAGCTCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAGGAGGTTCATCGTGGACA  
TCTTGCATATTGGACATTGGCTCTGATGTCACCCGAGTGGGCTGCTCCAATATGGCAGCAGTGTCAAGAATG  
AGTTCTCCCTCAAGACCTCAAGAGGAAGTCCGAGGTGGAGCGTGTCAAGGAGGATGCCGATCTGTCACGG  
GCACCATGACTGGGCTGGGACATCCAGTATGCCATGCCAATCTCAGAACAGCAGAGGGGCCGGCCCTGA  
GGGAGAATGTGCCACGGGCTATAATGATCGTACAGATGGAGACCTCAGGACTCTGTGGCCAGGTGGCTGCTA  
AGGCACGGGACACGGGATCCTAATCTTGCATTGGTGGCCAGGTAGAGTCAACACCTTGAAGTCCATTG  
GGAGTGGAGCCCCATGAGGACCATGTCCTGTGAGGAACTTTCAGCCAGATTGAGACGCTGACCTCCGTGTTCC  
AGAAGAAGTTGTGACGGGCCACATGTGAGCACCCCTGGAGCATAACTGTGCCACTCTGCATCAACATCCCTG  
GCTCATACGTCAGGTCAAACAGGCTACATTCTCAACTCGGATCAGACGACTTGAGAACATCCAGGATCTGT  
GTGCATGGAGGACCAACTGTGAGCAGCTGTGTGAATGTGCCGGCTCTCGTGTGAGTGTGCTACAGTG  
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGAGGACTACTGTGCTCAGAAAACACGGATGTGAAAC  
ATGAGTGTGTAATGCTGATGGCTCTACCTTGCCAGTGGCATGAAGGATTGCTCTTAACCCAGATGAAAAAA  
CGTGCACAAGGATCAACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGCCTCAACATGGAGGAGGCT  
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGCAAAACCTGCAAGCCGAGTGGACCAACTGTGAC  
AGCAGGACCATGGCTGTGAGCAGCTGTGTGAACACGGAGGATTCCCTGCTGCCAGTGTGCTAGAACGGCTCC  
TCATCAACGAGGACCTCAAGACCTGTCCTGGGGTGGATTACTGCTGCTGAGTGGCATGGTGTGAATACTCCT  
GTGTCACATGGACAGATCCTTGCCCTGTCAGTGTCTGAGGGACACGTGCTCCGAGCGATGGGAAGACGTGTG  
CAAAATTGGACTCTTGTGCTCTGGGGACACGGTTGTGAACATTGCTGTGAAGCAGTGAAGATTGTTGTG  
GCCAGTGTGTTGAAGGTTATATACTCCGTGAAGATGGAAAACCTGCAAGGAAAGATGTCTGCCAAGCTATAG  
ACCATGGCTGTGAACACATTGTGTGAACAGTGACGACTCATCACGTCAGTGTGCTGGAGGGATTCCGGCTCG  
CTGAGGATGGGAACGGCTGGCGAAGGAAGGATGTCTGCAAATCAACCCACCATGGCTGCAACACATTGTT  
ATAATGGGAATTCTACATCTGCAAATGCTCAGAGGATTGTTCTAGCTGAGGACGGGAAGACGGTGAAGAAAT  
GCACTGAAGGCCAATGACCTGGTCTTGATGGATCCAAGAGTCTTGGAGAAGAGAATTGAGGTG  
TGAAGCAGTTGTCACTGGAATTATAGATTCTGCTGACAATTCCCTAAAGCCGCTGAGTGGGCTGCTCCAGT  
ATTCCACACAGGTCCACACAGAGTTCACTCTGAGAAACTTCACAGCCAAAGACATGAAAAAAAGCCGTGGCC  
ACATGAAATACTGGAAAGGGCTATGACTGGGCTGCCCTGAAACACATGTTGAGAGAAGTTTACCCAAG  
GAGAAGGGGCCAGGCCCTTCCACAAGGTGCCAGACCGAGCCATTGTTGACCGACGGACGGGCTCAGGATG  
ACGTCCTGGAGTGGCCAGTAAGCCAAGGCCAATGGTATCACTATGATGCTGTGGGCTAGGAAAGCCATTG  
AGGAGGAACATACAAGAGATTGCTCTGAGCCCACAAACAAGCATCTTCTATGCCAGACTCAGCACAATGG  
ATGAGATAAGTAAAAACTCAAGAAAGGCATCTGTGAAGCTCTAGAAGACTCGATGGAAGACAGGACTCTCCAG  
CAGGGGAACGTGCCAAAACGGTCAACAGCCAACAGAATCTGAGCCAGTCACCATAAATATCCAAGACCTACTTT  
CCTGTTCTAATTGCACTGGTCAACACAGATATCTGTTGAGAAGACAATCTTACGGTCTACACAAAGCTTT  
CCCATTCAACAAACCTTCAGGAAGGCCCTTGGAAGAAAACAGATCAATGCAAATGTGAAAACCTTATAATGT  
TCCAGAACCTGCAACAGAAGTAAGAAAATTAAACACAGCGCTTAGAAGGAAATGACACAGAGAATGGAAGGCC  
TGGAAAATGCCCTGAGATAAGATGAAGATTAGAAAATGCCACACATTGTTAGTCATTGTTACGGATTACAAT  
GAACGCAGTGCAGAGCCCCAAAGCTCAGGCTATTGTTAAATCAATAATGTTGAGTAAAACAATCAGTACTGA  
GAAACCTGGTTGCCACAGAACAAAGACAAGAAGTATACTACACTAATGTTAGTAAATTTATCTAGGAAAAAAACCT  
TCAGAATTCTAAGATGAATTACCAAGGTGAGAATGAATAAGCTATGCAAGGTATTGTTGAAATATACTGTGGACAC  
AACTGCTTCTGCCCTCATCCTGCCATTGCAATCTCATTGACTATACGATAAAAGTTGCACAGTCTTACTT  
CTGAGAACACTGCCATAGGAAATGCTGTTTTGACTGGACTTACCTTGATATGTATATGGATGTATG  
CATAAAATCATAGGACATATGACTTGTGGAACAAGTTGAGTTTATACAATATAAAATTCAACACTTCAG

## **FIGURE 15**

MEKMLAGCFLLILGQIVLLPAEARERSGRSISRGRHARTHPOQTALLESSCENKRADLVFII  
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAV  
KMRHLSTGTMGLAIQYALNIAFSEAE GARPLRENVPRVIMIVTDGRPQDSVAEVAAKARD  
TGILIFAIVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHN  
CAHFCINIPGSYVCRKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNPVPGSFVCQCYSGYA  
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKPGC  
EHECVNMEESYYCRCHRGYTLDPNGKTCRSVDHCAQQDHGEQLCLNTEDSFVCQCSEGFLI  
NEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRS DGKTCAKLDSCALGDHGCE  
HSCVSSEDSFVCQCFCFGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFR LA  
EDGKRCRRKDVKSTHHGCEHICVNNNGNSYICKCSEG FVLAEDGRRCKCTEGPIDLVFVID  
GSKSLGEENFEVVKQFVTGIIDS LTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA  
HMKYMGKGSMTGLALKHM FERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN  
GITMYAVGVGKAIEELQEIA SEPTNKHLYAEDFSTMDEISEKLKKGICEALEDSDGRQDS  
PAGELPKTVQQPT ESEPVTINI QDLLSCNSFAVQHRYLFEE DNLLRSTQKL SHSTKPSGSPL  
EEKHDQCKCENLIMFQNL ANEEVRKLTQRLEEMTQRMEALENRLRYR

**Signal peptide:**

amino acids 1-23

**N-glycosylation site.**

amino acids 221-225

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 115-119, 606-610, 892-896

**Casein kinase II phosphorylation site.**

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,  
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,  
781-785, 819-823, 866-870

**N-myristoylation site.**

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,  
639-645, 690-696, 752-758, 792-798

**Amidation site.**

amino acids 314-318, 560-564, 601-605

**Aspartic acid and asparagine hydroxylation site.**

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,  
540-546, 581-587

## **FIGURE 16**

GGAGCCGCCCTGGGTGTCAGCGCTCGCTCCCGCAGCCTCCGCCGCGCAGCCTCG  
GCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCTGACTCCGTCCCAGGGAGGGC  
**CAT**GATTCCCTCCCCGGGCCCTGGTGACCAACTTGCTGCCGTTTGTTCTGGGCTGA  
GTGCCCTCGCGCCCCCTCGCGGCCAGCTGCAACTGCACCTGCCAACCCTGTCAG  
GCGGTGGAGGGAGGGAAAGTGGTCTTCCAGCGTGGTACACCTGCACGGGAGGTGCTTC  
ATCCCAGCCATGGGAGGTGCCCTTGATGTGGTCTTCAAACAGAAAGAAAAGGAGGATC  
AGGTGTTGTCTACATCAATGGGTACAACAAGCAAACCTGGAGTATCCTGGTCTACTCC  
ATGCCCTCCCGAACCTGTCCCTGCCGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCTA  
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGAAATCTAGGGCCACAGCATAAAACCT  
TAGAACTCAATGTACTGGTCTCCAGCTCCTCATCCTGCCGTCTCAGGGTGTGCCCAT  
GTGGGGCAAACGTGACCTGAGCTGCCAGTCTCCAAGGAGTAAGCCGCTGTCCAATACCA  
GTGGGATCGGCAGCTCCATCCTCAGACTTTCTTGACCCAGCATTAGATGTATCCGTG  
GGTCTTAAGCCTCACCAACCTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC  
AATGAGGTGGCACTGCCAATGTAATGTGACGCTGGAAGTGAGCACAGGCCCTGGAGCTGC  
AGTGGTTGCTGGAGCTGTTGGTACCCCTGGTGGACTGGGTTGCTGGCTGGCTGGTCC  
TCTTGTACCACCGCCGGCAAGGCCCTGGAGGAGCCAGCAATGATATCAAGGAGGATGCC  
ATTGCTCCCGACCCTGCCCTGGCCAAGAGCTCAGACACAATCTCAAGAATGGGACCC  
TTCCTCTGTCACCTCCGACGCCCTCCGGCCACCCATGGCCCTCCAGGCCTGGTCAT  
TGACCCCCACGCCAGTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT  
GGGGCCACCCCTCAACCAATATCCCCCATCCCTGGTGGGTTCTCCTCTGGCTTGAGCCG  
CATGGGTGCTGTGCCTGTGATGGTGCCCTGCCCAGAGTCAGCTGGCTCTGGT**TATGATGAC**  
CCCACCACTATTGGCTAAAGGATTGGGTCTCTCCTATAAGGGTACCTCTAGCAC  
AGAGGCCTGAGTCATGGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCACCTCTC  
TTTACTGTGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA  
AGTGGATCTGGAATTGGGAGGAGCCTCACCCACCCCTGACTCCTCTTATGAAGCCAGCTG  
CTGAAATTAGCTACTCACCAAGAGTGAGGGCAGAGACTTCCAGTCAGTCACTGAGTCTCCAGGC  
CCCCCTGATCTGACCCACCCCTATCTAACACCAACCCCTGGCTCCACTCCAGCTCCCTGT  
ATTGATATAACCTGTCAGGCTGGCTGGTTAGGTTTACTGGGAGGATAGGAAATCTC  
TTATTAACATGAAATATGTGTTTTCAATTGCAAATTAAATAAGATAACATAA  
TGTTGTATGAAAAA

## **FIGURE 17**

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS  
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDGPY  
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSKP  
AVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGT  
AQCNVTLLEVSTGPGAAVVAGAVVGTILVGLGLLAGLVLLYHRRGKALEEP  
PANDIKEDAIAAPRTLWPWKSSDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSS  
SQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 245-267

**N-glycosylation site.**

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

**N-myristoylation site.**

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,  
262-268, 308-314, 363-369, 364-370

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 164-175

## **FIGURE 18**

CGCCACCACTGGGCCACCGCCAATGAAACGCCTCCGCTCCTAGTGGTTTTCCACTTTG  
TTGAATTGTCCTATACTCAAATTGCACCAAGACACCTGTCTCCAAATGCAAATGTGA  
AATACGCAATGGAATTGAAGCCTGCTATTGCAACATGGGATTTCAGGAAATGGTGTACAA  
TTTGTGAAGATGATAATGAATGTGGAAATTAACTCAGTCCTGTGGCAGAACATGCTAATTGC  
ACTAACACAGAAGGAAGTTATTGTATGTGTACCTGGCTCAGATCCAGCAGTAACCA  
AGACAGGTTTATCACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACGTGCCATT  
TAGATAATGTCTGTATAGCTGCAAATATTAATAAAAACCTTAACAAAAATCAGATCCATAAAA  
GAACCTGTGGCTTGTACAAGAAGTCTATAGAAAATTCTGTGACAGATCTTCACCAACAGA  
TATAATTACATATAGAAAATTAGCTGAATCATCTTCACTACTAGGTTACAAGAACAAACA  
CTATCTCAGCCAAGGACACCCCTTCTAACTCAACTCTTACTGAATTGTAAAAACCGTGAAT  
AATTTGTTCAAAGGGATACTTGTAGTTGGACAAGTTATCTGTGAATCATAGGAGAAC  
ACATCTTACAAAACATGCACACTGTTGAACAAAGCTACTTAAAGGATATCCCAGAGCTTCC  
AAAAGACCACAGAGTTGATAACAAATTCAACGGATATAGCTCTCAAAGTTTCTTTTGAT  
TCATATAACATGAAACATATTCATCCTCATATGAATATGGATGGAGACTACATAAATATATT  
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATA  
AGAGTATTGGTCTTGTCTTCATCATCTGACAACCTTCTTATTGAAACCTCAAATTATGAT  
AATTCTGAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTCAGTCTCAATGAGCTCAAACCC  
ACCCACATTATATGAACTTGAAAAAAATAACATTACATTAAGTCATCGAAAGGTACAGATA  
GGTATAGGAGTCTATGTGCATTGGAAATTACTCACCTGATACCATGAATGGCAGCTGGTCT  
TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCT  
GACACATTTGCAATTGATGTCCTCTGGCCTTCCATTGGTATTAAAGATTATAATATT  
TTACAAGGATCACTCAACTAGGAATAATTATTCACTGATTGTCTGCCATATGCATT  
ACCTTCTGGTTCTTCAGTCAAAGCACCAGGACAACAATTCAACAAAATCTTGCTG  
TAGCCTATTCTTGCTGAACTGTTCTTGTGGATCAATACAAACTAATAAGCTCT  
TCTGTTCAATCATTGCCGGACTGCTACACTACTCTTTAGCTGCTTGCATGGATGTGC  
ATTGAAGGCATACATCTCATCTGATTGGTGTGTCATCTACAACAAAGGGATTGGCA  
CAAGAATTTTATATCTTGCTATCTAACGCCAGCCGTGGTAGTTGGATTTCGGCAGCAC  
TAGGATACAGATATTATGGCACAACCAAGTATGTTGGCTTAGCACCGAAAACAAC  
TGGAGTTTATAGGACCAGCATGCCTAATCATTCTGTTAATCTCTTGGCTTGGAGTCAT  
CATATACAAAGTTTCGTCAACTGCAGGGTTGAAACCAGAAGTTAGTTGCTTGGAGAAC  
TAAGGTCTTGTGCAAGAGGAGCCCTCGCTTTCTGTTCTCGGCACCACTGGATCTT  
GGGGTTCTCCATGTTGTGCACGCATCAGTGGTTACAGCTACCTCTCACAGTCAGCAATGC  
TTTCAGGGGATGTTCATTTTTATTCTGTGTTTATCTAGAAAGATTCAAGAAGAAT  
ATTACAGATTGTTCAAATGCCCCCTGTTGGATGTTAAGGTAAACATAGAGAAC  
GTGGATAATTACAACGTGACAAAAATAAAATTCCAAGCTGTGGATGACCAATGTATAAAA  
TGACTCATCAAATTATCAATTAAACTACTAGACAAAAAGTATTAAATCAGTT  
GTTTATGCTATAGGAACACTGTAGATAATAAGGAAAATTATGTATCATATAGATAACTATGT  
TTTCTATGTGAAATAGTCTGTCAAAATAGTATTGAGATATTGGAAAGTAATTGGTT  
CTCAGGAGTGTATCACTGCACCCAAAGGAAAGATTTCTAACACGAGAAGTATATGAA  
TGTCTGAAGGAAACCACGGCTGATATTCTGTGACTCGTGTGCTTGAACACTAGTCC  
CCTACCACCTCGTAATGAGCTCCATTACAGAAAGTGGAACATAAGAGAACATGAAGGGCAGA  
ATATCAAACAGTGAAAAGGAATGATAAGATGTATTGAAATGAACTGTTCTGTAGAC  
TAGCTGAGAAATTGTTGACATAAAATAAGAATTGAAGAACACATTTCACATTGAA  
TTGTTCTGAACTTAAATGTCCACTAAACAACTTAGACTCTGTTGCTAAATCTGTTCTT  
TTCTAATATTCTAAAAAAAAAGGTTACCTCCACAAATTGAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 19**

MKRLPLLVVFSTLLNCSYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC  
GNLTQSCGENANCTNTEGSYYCMCVPGRSSSNQDRFITNDGTVCIENVANCHLDNVCIAA  
NINKTLTKIRSIKEPVALLQEVRNSVTDLSPTDIITYIEILAESSLLGYKNNTISAKDTL  
SNSTLTFVKTVNNFVQRDTVVWDKLSVNHRRTHTKLMHTVEQATLRISQSFQKTTEFDT  
NSTDIALKVFFFDSYNMKHIHPHMNMDGYINIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS  
SSDNFLLKPQNYDNSEEERVISSVISVSMSSNPPTLYELEKITFTLSRKVTDRYRSLCAF  
WNYSPDTMNGWSSEGCELTYSNETHTSCRNCNLTHFAILMSSGPSIGIKDYNILTRITQLG  
IIISLICLAICIFTWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCIIAGL  
LHYFFLAAFAWMCIEGIHLYLIVGVIVNKGLHKNFYIFGYLSPA VVGFSAALGYRYYGT  
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA  
LALLFLLGTTWIFGVLVHVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV  
PCCFGCLR

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,  
648-664

**N-glycosylation site.**

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,  
188-192, 249-253, 381-385, 395-399

**Glycosaminoglycan attachment site.**

amino acids 49-53

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 360-364

**Casein kinase II phosphorylation site.**

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,  
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,  
346-350, 608-612

**Tyrosine kinase phosphorylation site.**

amino acids 36-44, 669-677, 670-678

**N-myristoylation site.**

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,  
434-440, 480-486, 521-527

**Aspartic acid and asparagine hydroxylation site.**

amino acids 75-87

## **FIGURE 20**

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATAATTTCCAAAGNG  
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATAAGAGTAT  
TGGTCCCTTGCTTCATCATCTGACAACCTCTTATTGAAACCTCAAAATTATGATAATTCT  
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTCACTGAGCTCAAACCCACCCAC  
ATTATATGAACTTGAAAAAACATTACATTAAGTCATCGAAAGGTACAGATAGGTATA  
GGAGTCTATGTGGCATTTGGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG  
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA  
TTTGCAATTGATGTCCTCTGGCCTTCCATTGGTATTAAAGATTATAATATTCTTACAA  
GGATCACTCAACTAGGAATAATTATTCACTGATTGTCTGCCATATGCATTTACCTTC  
TGGTTCTTCAGTGAAATTCAAAGCACCAGGA

## **FIGURE 21**

GCTCCCAGCCAAGAACCTGGGGCCGCTGCGCGGTGGGGAGGAGTCCCCGAAACCCGGCCG  
CTAAGCGAGGCCTCCTCCCTCCCGCAGATCCGAACGGCCTGGCGGGGTCAACCCGGCTGGGA  
CAAGAACGCCCGCCTGCCTGCCCGGGGCCGGAGGGGGCTGGGCTGGGCCGGAGGCGG  
GGTGTGAGTGGGTGTGCGGGGGCGAGGCTTGATGCAATCCCATAAGAAATGCTCGGG  
TGTCTGGCACCTACCCGTGGGCCCCGTAAGGCGCTACTATATAAGGCTGCCGGCCGGAG  
CCGCCGCGCCGTAGAGCAGGAGCGCTCGTCCAGGATCTAGGCCACGACCATCCAAACCC  
GGCACTCACAGCCCCAGCGCATCCGGTCGCCAGCCTCCGCACCCCCATGCCGG  
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGGTGGTCCACGTATGG  
ATCCTGGCCGGCCTCTGGCTGGCGTGGCCGGCGCCCCCTCGCCTTCTCGGACGCGGGCC  
CCACGTGCACTACGGCTGGGCGACCCCATCCGCTGCACCTGTACACCTCCGGCCCCC  
ACGGGCTCTCCAGCTGCTTCCGCACTCGTGGACGGAGATCAAGGCAGTCGCTCTCGGGACCGTGGCCATCAAGGG  
CAGAGCGCGCACAGTTGCTGGAGATCAAGGCAGTCGCTCTCGGGACCGTGGCCATCAAGGG  
CGTGCACAGCGTGCAGTACCTCTGCATGGCGCCAGGCAAGATGCAGGGCTGCTTCAGT  
ACTCGGAGGAAGACTGTGCTTCGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA  
TCCGAGAAGCACGCCCTCCGGTCTCCCTGAGCAGTGCAAACAGCGGAGCTGTACAAGAA  
CAGAGGCTTCTTCCACTCTCTCATTCCGCCCCATGCTGCCCTGGAGACCGACAGCATG  
AGGACCTCAGGGGCCACTTGGAAATCTGACATGTTCTTCGCCCCCTGGAGACCGACAGCATG  
GACCCATTGGGCTTGTACCGGACTGGAGGCCGTGAGGAGTCCAGCTTGAGAAGTAACT  
GAGACCATGCCGGGCTTCACTGCTGCCAGGGCTGTGGTACCTGCAGCGTGGGACG  
TGCTTCTACAAGAACAGTCCTGAGTCCACGTTCTGTTAGCTTAGGAAGAACATCTAGAA  
GTTGTACATATTCAAGAGTTTCCATTGGCAGTGCAGTTCTAGCCAATAGACTTGTCTGAT  
CATACATTGTAAGCCTGTAGCTGCCAGCTGCTGCCGGCCCCATTCTGCTCCCTCGA  
GGTTGCTGGACAAGCTGCTGCACTGTCAGTTCTGCTGAATACCTCCATCGATGGGAAC  
TCACTCCTTGGAAAATTCTTATGTCAAGCTGAAATTCTCTAATTTCATCACTTC  
CCCAGGAGCAGCCAGAACAGACAGGAGTAGTTAATTCAAGAACAGGTGATCCACTCTGTA  
AACACAGCAGTAAATTCACTCAACCCATGTGGAATTGATCTATCTACTTCCAGGG  
ACCATTGCCCTCCCAAATCCCTCCAGGCCAGAACCTGACTGGAGCAGGCATGGCCCACCGAG  
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACCTGAGAACATTCCCC  
CTGAGGCCAGTTCTGCATGGATGCTGCTGAGAATAACTTGCTGCTCCGGTGTACCTGC  
TTCCATCTCCAGGCCACCAGCCCTCTGCCACCTCACATGCCTCCCCATGGATTGGGCCT  
CCCAGGCCCCCACCTTATGTCAACCTGCACCTCTGTTCAAAAATCAGGAAAAGAAAAGAT  
TTGAAGACCCCAAGTCTGTCAATAACTTGCTGTTGGAAGCAGGGGGAGACCTAGAAC  
CCTTCCCCAGCACTGGTTTCCAACATGATATTATGAGTAATTATTTGATATGTACA  
TCTCTTATTTCTTACATTATTATGCCCAAATTATATTATGTATGTAAGTGAGGTTG  
TTTGTATATTAAAATGGAGTTGTTGT

## **FIGURE 22**

MRSGCVVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWDPIRLRHLYTSGPHGLSSCFLRI  
RADGVVDCARGQSAHSLLEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEE  
EIRPDGYNVYRSEKHLPLVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD  
MFSSPLETDSMDPFGLVTGLEAVRSPSFEK

**Signal peptide:**

amino acids 1-22

**Casein kinase II phosphorylation site.**

amino acids 78-82, 116-120, 190-194, 204-208

**N-myristoylation site.**

amino acids 15-21, 54-60, 66-72, 201-207

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 48-59

## **FIGURE 23**

CCCAGAACGTTCAAGGGCCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCCTGACCTCCTCA  
GAGCAGCCGGCTGCCGCCGGGAAGATGGCGAGGAGGAGCCACCGCCTCCTGCTG  
CTGCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTTCTGCCCAAA  
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTAGCCTGCAAAACCCCAA  
AGAAGACTGTTCCCTCAGATTAGAGTGGAAAGAAACTGGGTGGAGTGTCTCCTTGCTAC  
TATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGATTTCAATATCCG  
GATCAAAAATGTGACAAGAAGTGATGCCGGAAATATCGTTGTGAAGTTAGTGCCTCATCTG  
AGCAAGGCCAAACCTGGAAGAGGATAACAGTCACACTGGAAGTATTAGTGGCTCCAGCAGTT  
CCATCATGTGAAGTACCTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA  
CAAAGAAGGAAATCCAGCTCCTGAATACACATGGTTAAGGATGGCATCCGTTGCTAGAAA  
ATCCCAGACTGGCTCCAAAGCACCAACAGCTCATACACAATGAATACAAAAACTGGAAC  
CTGCAATTAAACTGTTCCAAACTGGACACTGGAGAATATTCCGTGAAGCCGCAATT  
TGTTGGATATCGCAGGTGTCCTGGAAACGAATGCAAGTAGATGATCTAACATAAGTGGCA  
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTCCGTTGTGGCCTTGGTGTATGCTAT  
GCTCAGAGGAAAGGCTACTTTCAAAAGAAACCTCCTCCAGAAGAGTAATTCTCATCTAA  
AGCCACGACAATGAGTGAATGTGCAGTGGCTACGCCTGTAATCCCAGCAGTTGGAAGG  
CCGGCGGGCGGATCACGAGGTCAGGAGTTCTAGACCAGTCTGGCAATATGGTAAACCC  
CATCTCTACTAAAATACAAAAATTAGCTGGCATGGTGGCATGTGCCCTGCAGTTCCAGCTGC  
TTGGGAGACAGGAGAACACTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC  
CACTGCAGTCCAGCCTGGTAACAGAGCAAGATTCCATCTCAAAAAATAAATAAATA  
AATAAATACTGGTTTACCTGTAGAATTCTTACAATAATAGCTTGATATT

## **FIGURE 24**

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKQQVVTAVEYQEAILACKTPKKTVSSRLE  
WKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEED  
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKD GIRLLENPRILGSQST  
NSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVA  
LVISVCGLGV CYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALWKA AAGGSRGQEF

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 130-144, 238-258

**N-glycosylation site.**

amino acids 98-102, 187-191, 236-240, 277-281

**Casein kinase II phosphorylation site.**

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

**N-myristoylation site.**

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

**Amidation site.**

amino acids 226-230

## **FIGURE 25**

GACATCGGAGGTGGCTAGCACTGAAACTGCTTTCAAGACGAGGAAGAGGAGGAGAAAGAG  
AAAGAAGAGGAAGATGTTGGCAACATTATTTAACATGCTCCACAGCCCGGACCTGGCAT  
CATGCTGCTATTCTGCAAATACTGAAGAAGCATGGATTAAATATTTACTTCTAAATAA  
ATGAATTACTCAATCTCCTATGACCACACTACATACACTCCACCTCAAAAAGTACATCAATA  
TTATATCATTAAAGGAAATAGTAACCTCTTCTCCAATATGCATGACATTGGACAATG  
CAATTGTGGCACTGGCACTTATTTCAGTGAAGAAAAACTTGTGGTTATGGCATTCA  
TTTGACAAATGCAAGCATCTCCTTATCAATCAGCTCTATTGAACTTACTAGCACTGACTG  
TGGAATCCTTAAGGGCCCATTACATTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT  
CCGAATTCACTGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG  
TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTGGTTACACCCAGATCCATTAT  
ATGGAAGCCTACAGTGGATTGTAATGATTAGGTCTTTAACCTTCCCAGCCAGATTGCC  
AGCTAACACACAGATTCTCTCCTACAGACTAACAAATATTGAAATACTCCACAG  
ACTTTCCAGTAAACCTACTGGCCTGGATTATCTCAAAACAATTATCTCAGTCACCAAT  
ATTAATGTAAGGAAAGATGCCTCAGCTCCTTCTGTGTACCTAGAGGAAACAAACTACTGA  
ACTGCCTGAAAATGTCTGCGAACTGAGCAACTACAAGAACTCTATATTAACTACAACT  
TGCTTCTACAATTTCACCTGGAGCCTTATTGGCCTACATAATCTCTCGACTTCATCTC  
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTGATGCTCTCCAAATCTAGAGAT  
TCTGATGATTGGGAAAGATCCAATTATCAGAACGAACTGAACTTTAACCTCTTATCA  
ATCTTCGCAGCCTGGTTATAGCTGGTATAAACCTCACAGAAATACCGATAACGCCTGGTT  
GGACTGGAAAACCTAGAAAGCATCTCTTTACGATAACAGGCTTATTAAAGTACCCCATGT  
TGCTCTCAAAAGTTGTAATCTCAAATTGGATCTAAATAAAACCTTAAATAGAA  
TACGAAGGGGTGATTAGCAATATGCTACACTAAAAGAGTTGGGATAAATAATATGCCT  
GAGCTGATTCCATCGATAGTCTGCTGTGGATAACCTGCCAGATTAAAGAAAATAGAAGC  
TACTAACACCCCTAGATTGTCTTACATTCAACCCCAATGCATTTCAGACTCCCCAAGCTGG  
AATCACTCATGCTGAACAGCAATGCTCAGTGCCCTGTACCATGGTACCATGGTCTG  
CCAAACCTCAAGGAAATCAGCATACACAGTAACCCATCAGGTGTGACTGTGTCATCCGTTG  
GATGAACATGAACAAAACCAACATTGATTGATGGAGCCAGATTCACTGTTGCGTGGACC  
CACCTGAATTCCAAGGTCAAGATGTTGGCAAGTGCATTTCAGGGACATGATGAAATTGT  
CTCCCTCTTATAGCTCCTGAGAGCTTCTTCTAAATCTAAATGTAGAAGCTGGAGCTATGT  
TTCCTTCACTGTAGAGCTACTGCAGAACACAGCCTGAAATCTACTGGATAACACCTTCTG  
GTCAAAAACCTTGCCTAATACCCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAAACACTA  
GATATAATGGCGTAACCTCCAAAGAAGGGGTTATATACTTGTATAGCAACTAACCTAGT  
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTCCACAAAGATAACAAATG  
GCTCTTGAATATTAAAAGAGATATTCAAGGCCAATTCAAGTTGGTGTCTGGAAAGCA  
AGTTCTAAAATTCTCAAATCTAGTGTAAATGGACAGCCTTGTCAAGACTGAAATTCTCA  
TGCTGCGCAAAGTGCCTGAATACCATCTGATGTCAGGTATATAATCTTACTCATCTGAATC  
CATCAACTGAGTATAAAATTGTATTGATATTCCCACCATCTATCAGAAAAACAGAAAAAAA  
TGTGTAATGTCACCACCAAGGTTGCACCCCTGATCAAAAAGAGTATGAAAAGAATAATAC  
CACACACATTGGCCTGTCTGGAGGCCTTCTGGGATTATTGGTGTGATATGTCTTATCA  
GCTGCCTCTCCAGAAATGAACTGTCAGTGGTGGACACAGCTATGTGAGGAATTACTTACAG  
AAACCAACCTTGCATTAGGTGAGCTTATCCTCTGTATAATCTGGGAAGCAGGAAA  
AGAAAAAAAGTACATCACTGAAAGTAAAAGCAACTGTTAGGTTACCAACAAATATGTCCT  
AAAAACCAAGGAAACCTACTCCAAAATGAAC

## **FIGURE 26**

MKDMLPLRIHVLLGLAITTLVQAVDKVDCPRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT  
FPARLPANTQILLQTNNAKIEYSTDFPVNLTLGDLDSQNNLSSVTNINVKKMPQLLSVYLE  
ENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHNLLRLHNSNRQMINSKWFDA  
LPNLEILMIGENPIIRIKDMNFKPLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRL  
IKVPHVALQKVNLKFDDLNKNPINRIRRQDFSNMLHLKELGINNMPELISIDSALVDNLPD  
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNSNALSALYHTIESLPNLKEISIHSPIRC  
DCVIRWMNMNKTNIRFMEEPDSLFCVDPPEFQGQNVHQVFRDMMEICLPLIAPESFPSNLNV  
EAGSYVSFHCRATAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLINGVTPKEGGLYTC  
IATNLVGAIDLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSKASSKILKSSVKWTAFV  
KTENSHAAQSARI PSDVKVYNLTHLN PSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE  
YEKNNTTTLMACLGGILLGIIGVICLISCLSPEMNC DGGHSYVRNYLQKPTFALGELYPP LIN  
LWEAGKEKSTS LKV KATV IGLPTNMS

**Signal sequence:**

amino acids 1-22

**Transmembrane domain:**

amino acids 633-650

**N-glycosylation site.**

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,  
608-612, 624-628, 625-629

**Casein kinase II phosphorylation site.**

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

**Tyrosine kinase phosphorylation site.**

amino acids 570-579

**N-myristoylation site.**

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,  
491-497, 492-498, 634-640, 702-708

**Cell attachment sequence.**

amino acids 277-280

## **FIGURE 27**

GCCCCGGACTGGCGAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG  
CTGCAGCCTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTAC  
CACGCTTGTGGAGTAGATGAGGAATGGGCTCGTGAATTATGCTGACATTCCAGCATGAATCT  
GGTAGACCTGTGGTTAACCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTTGTTCTTA  
TGATACTGTGCTTCATTCTGCCAGTATGTGTCCAAGGGCTGTCTTGTCTCCTCTGGG  
GGTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTCCTCCTGA  
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTAAAGG  
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAATGGCATTGAGTTATCGATGAGCAT  
GCCTCAAAGGAGTAGCTGAAACCTTGAGACTCTGGACTTGTCCGACAATCGGATTCAAAG  
TGTGCACAAAATGCCTTCATAAACCTGAAGGCCAGGGCAGAATTGCCAACAAACCCCTGGC  
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCAATCATGAGACAGCCCAC  
AACGTGATCTGTAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC  
CAACGACGCTGACCTTGTAAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA  
TGTTGGCTGGTCACTATGGTGAATCTCATATGTGGTATATTATGTGAGGCAAATCAGGAG  
GATGCCCGGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGAGAAGAAAGCAGATGA  
ACCTGATGATATTAGCACTGTGGTATAGTGTCCAAACTGACTGTCAATTGAGAAAGAAAGAAA  
GTAGTTGCGATTGCACTAGAAATAAGTGGTTACTTCTCCCATCATTGAAACATTTGAA  
ACTTGTATTCAGTTTTGAAATTATGCCACTGCTGAACCTTAACAAACACTACAACA  
TAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTACCCCCGATGGTATATTCTGAGT  
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTAATAATGAAATTATTTTTT  
AATTAAAAGCAAATAAGCTTAACCTTGAACCAGGGAAAAAAAAAAAAAAACA

## **FIGURE 28**

MNLVDLWLTRSLSMCLLQSFVLMILCFHSASMC PKGCLSSSGGLNVTC SNANLKEIPRDL  
PPETVLLYLDQNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDSLDR  
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHEAHNVICKTSVLDEHAGRPF  
NAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK  
ADEPDDISTVV

**Signal sequence:**

amino acids 1-33

**Transmembrane domain:**

amino acids 205-220

**N-glycosylation site.**

amino acids 47-51, 94-98

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 199-203

**Casein kinase II phosphorylation site.**

amino acids 162-166, 175-179

**N-myristoylation site.**

amino acids 37-43, 45-51, 110-116

## **FIGURE 29**

ACCGAGCCGAGCGAACGAAGGCCGCCCCGAGATGAGGTGAGCAAGAGGATGCTGGCGGG  
GGCGTGAGGAGCATGCCAAGCCCCCTCTGGCCTGCTGGCAGCCCATTCTCTGCTGGTGCT  
GGGCTCAGTGTGTCAGGCTGGCCACGGCTGCCGCCGCTGCGAGTGCTCCGCCAGG  
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTGCGACTCCCCGAGGGCATCCCCACCGAG  
ACGCGCTGCTGGACCTAGGCAAGAACCGCATAAAACGCTCAACCAGGACGAGTTGCCAG  
CTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTAGGCCTGGAGGCCGGCG  
CCTTCAACAAACCTCTCAACCTCCGGACGCTGGGTCTCCGAGCAACCGCCTGAAGCTCATC  
CCGCTAGGCGTCTTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAGAT  
CGTTATCCTACTGGACTACATGTTCAGGACCTGTACAACCTCAAGTCAGTGGAGGTTGGCG  
ACAATGACCTCGTCTACATCTCACCAGCGCCTCAGCGGCCTCAACAGCCTGGAGCAGCTG  
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGGCGCTGCCCACCTGCACGGCCT  
CATCGTCTGAGGCTCGGCACCTCAACATCAATGCCATCCGGACTACTCCTTAAGAGGC  
TGTACCGACTCAAGGTCTGGAGATCTCCACTGGCCCTACTTGGACACCATGACACCCAAC  
TGCCTCTACGGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC  
CTACCTGGCCGTCCGCCACCTAGTCTATCTCGCTTCTCAACCTCTCCTACAACCCCCATCA  
GCACCATTGAGGGCTCCATGTTGATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGGC  
GGGCAGCTGGCGTGGTGGAGGCCCTATGCCTTCCGGCCTCAACTACCTGCGCGTGTCAA  
TGTCTCTGGCAACCAGCTGACCAACTGGAGGAATCAGTCTTCACTCGGTGGCAACCTGG  
AGACACTCATCCTGGACTCCAACCGCTGGCCTGCGACTGTCGGCTCCTGTGGGTGTTCCGG  
CGCCGCTGGCGCTCAACTTCAACCGGAGCAGGCCACGTGCGCCACGCCAGTTGTCCA  
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCAACTACTTCACCTGCCGCCGCG  
CCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTGTGGACGAGGCCACCGGTGAGTT  
GTGTGCCGGCGATGGCGACCGGCCCATCCTCTGGCTCTCACCCGAAAGCACCT  
GGTCTCAGCCAAGAGCAATGGCGGCTCACAGTCTCCCTGATGGCACGCTGGAGGTGCGCT  
ACGCCCAAGGTACAGGACAACGGCACGTACCTGTGCATCGCGGCCAACGCCGGCAACGAC  
TCCATGCCGCCACCTGCATGTGCGCAGCTACTGCCACTGGCCCCATCAGCCCAACAA  
GACCTTCGCTTTCATCTCCAACCAGCGGGCGAGGGAGAGGCCAACAGCACCGGCCACTG  
TGCCTTCCCTTCGACATCAAGACCTCATCATGCCACCACATGGCTCATCTCTTTC  
CTGGCGTCGCTCTTCTGCCCTGGTGTGCTGTTCTGGAGCCGGCAAGGGCAACAC  
AAAGCACAACATCGAGATCGAGTATGTCCCCGAAAGTCGGACGCAGGCATCAGCTCCGCC  
ACGCCCAAGGTACAGGACAACGGCACGTACCTGTGCATCGCGGCCAACGCCGGCAACGAC  
GGCGGCCGGCAGGGGAAGGGGCTGGCGCCACCTGCTCACTCTCCAGTCCTCCACCTC  
CTCCCTACCCCTCACACAGTTCTCTTCTCCCTCCGCCCTCCGCTCCCTGCTGCCCG  
CCAGCCCTCACCACCTGCCCTCTTCTACAGGACCTCAGAACGCCAGACCTGGGACCCCA  
CCTACACAGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCCAGAGTC  
ATAATTCAATAAAAAAGTTACGAACCTTCTCTGTAACCTGGTTCAATAATTATGGATTT  
TATGAAAACCTGAAATAATAAAAAAGAGAAAAAAACTAAAAAAAAAAAAAA

## **FIGURE 30**

MQVKRMLAGGVRSMPSPLLACWQPILLVLGSVLSGSATGCPPCECSAQDRAVLCHRKCF  
VAVPEGIPTETRLLDLGKNRIKTLNQDEFASFPHLEELELNENIVSAVEPGAFNNLFNLRTL  
GLRSNRKLIPLGVFTGLSNLTKQDISENKIVILLDYMFQDLYNLKSLEVGDNDLVYISHRA  
FSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKVLEISH  
WPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFNLNSYNPISTIEGSMLHEL  
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVNVSGNQLTTLEESVFHSVGNLETLILDSNPLA  
CDCRLLWVFRRRWRLLNFNRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV  
FVDEGHTVQFVCRADGDPPPAILWLSPRKHLVSAKSNGRLTVFPDGTLLEVRYAQVQDNGTYL  
CIAANAGGNDNSMPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI  
IATTMGFISFLGVVLFCVLFLWSRGKGNTKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 556-578

**N-glycosylation site.**

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,  
492-496, 505-509, 526-530, 542-546

**Casein kinase II phosphorylation site.**

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,  
607-611

**Tyrosine kinase phosphorylation site.**

amino acids 590-598

**N-myristoylation site.**

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,  
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 32-43

## **FIGURE 31**

CCCACGCGTCCGCACCTCGGCCCGGGCTCCGAAGCGGCTCGGGGGGCCCTTCGGTCAAC  
ATCGTAGTCCACCCCTCCCCATCCCCAGCCCCGGGGATTCAAGGCTGCCAGCGCCCAGCC  
AGGGAGCCGGCGGGAAAGCGCG**AT**GGGGGCCAGCCGCTCGCTCCTGCTCCTGC  
TGTCGCCTGCTGGCGCCGGCGGGCCAACCTCTCCAGGACGACAGCCAGCCCTGG  
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTCAAGTGCAAGTGAAAGATCA  
CGAGGACTCATCCCTGCAATGGTCAACCCTGCTCAGCAGACTCTACTTTGGGAGAAGA  
GAGCCCTTCGAGATAATCGAATTCAAGCTGGTACCTCTACGCCAACGAGCTCAGCATCAGC  
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGT  
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAACCCATCATCACTGGTT  
ATAAACTTCATTACGGGAAAAAGACACAGCCACCCCTAAACTGTCAGTCTCTGGGAGCAAG  
CCTGCAGCCCGGCTCACCTGGAGAAAGGGTGACCAAGAACCTCACGGAGAACCAACCCGCAT  
ACAGGAAGATCCAATGGTAAAACCTTCACTGTCAGCAGCTGGTACATTCCAGGTTACCC  
GGGAGGATGATGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC  
AGATCCACCTCTCAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC  
TCCCCATCCTCGTGAGGGCAGAAGCTGTTGCTACACTGTGAGGGCGCGCAATCCAGTCC  
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT  
GCCCTGATCTCCCTTCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCA  
CAACATGGGCAGCTACAAGGCCTACTACACCCCTCAATGTTAATGACCCAGTCCGGTGCCT  
CCTCCTCCAGCACCTACCACGCCATCATCGTGGGATCGTGGCTTCATTGTCTCCTGCTG  
CTCATCATGCTCATCTTCCCTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA  
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCG  
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTCA**T****A**GGCGCCTGCCACTTCCTGC  
GCCCCCAAGGGGCCCTGTGGGACTGCTGGGCCGTACCAACCCGGACTTGTACAGAGCAA  
CCGCAGGGCCGCCCTCCCGCTTGTCCCCAGCCCACCCACCCCGTACAGAACGTCTGC  
TTGGGTGCGGTTTGACTCGGTTGGAATGGGGAGGGAGGAGGGCGGGGGAGGGAGGG  
TTGCCCTCAGCCCTTCCGTGGCTCTGCATTGGTTATTATTATTTGTAACAATCC  
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGGCCCTGGGTGAGAAAAGCAAAAACA  
AACAAAAAACAA

## **FIGURE 32**

MGAPAASLLLLLFFACCWAPGGANLSQDDSQWPWTSDETVVAGGTVVLCQVKDHEDSSLQW  
SNPAQQTLYFGEKRALRDNRQLQVTSTPHELSIISNVALADEGEYTCSIFTMPVRTAKSLV  
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGQELHGEPTRIQEDPNGK  
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ  
KLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA  
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLIRHKGTYLTHEAKGSDD  
APDADTAIINAEGGQSGGDDKKEYFI

**Signal sequence:**

amino acids 1-20

**Transmembrane domain:**

amino acids 331-352

**N-glycosylation site.**

amino acids 25-29, 290-294

**Casein kinase II phosphorylation site.**

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

**N-myristoylation site.**

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,  
306-310, 334-340, 360-364, 385-389, 386-390

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## **FIGURE 33**

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCCTTCTTCTCCTTCCTGG  
CTTCGGACATTGGAGCACTAAATGAACCTGAATTGTGTCTGTGGCGAGCAGGATGGTCGCTG  
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGCTTAAAAATGCTGCTTGGATTCTGTT  
GCTGGAGACGTCTCTTGCCGCTGGAAACGTTACAGGGGACGTTGCAAAGAGAAGA  
TCTGTTCTGCAATGAGATAGAAGGGACCTACACGTAGACTGTGAAAAAAAGGGCTTCACA  
AGTCTGCAGCGTTCACTGCCCGACTTCCCAGTTACCATTTATTCATGGCAATT  
CCTCACTCGACTTTCCCTAATGAGTTGCTAACCTTATAATGCGGTTAGTTGCACATGG  
AAAACAATGGCTTGCATGAAATCGTCCGGGGCTTTCTGGGCTGCAGCTGGTAAAAGG  
CTGCACATCAACAACAAGATCAAGTCTTTCGAAAGCAGACTTTCTGGGCTGGACGA  
TCTGGAATATCTCCAGGCTGATTTAATTATTACGAGATATAGACCCGGGGCCTCCAGG  
ACTTGAACAAGCTGGAGGTGCTCATTTAAATGACAATCTCATCAGCACCCCTACCTGCCAAC  
GTGTTCCAGTATGTGCCATACCCACCTCGACCTCCGGTAACAGGCTGAAAACGCTGCC  
CTATGAGGAGGTCTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCC  
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAACATTCCAAGAATGCC  
CTGATCGGCCGAGTGGTCTGCGAAGCCCCCACCAGACTGCAGGGTAAAGACCTCAATGAAAC  
CACCGAACAGGACTTGTGCTTGGAAAAACCGAGTGGATTCTAGTCTCCGGCGCCCCCTG  
CCCAAGAAGAGACCTTGTCTGGACCCCTGCCAACTCCTTCAAGACAAATGGCAAGAG  
GATCATGCCACACCAGGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT  
CAAATCAGACCCACAGCAGCGATAGCGACGGTAGCTCAGGAACAAACCTTAGCTAAC  
GTTTACCTGCCCTGGGGCTGCAGCTGCACCACATCCAGGGTGGTTAAAGATGAAC  
TGCAACAACAGGAACGTGAGCAGCTGGCTGATTGAAGCCAAGCTCTAACGTGCAGGA  
GCTTTCTACGAGATAACAGATCCACAGCATCCGAAATCGCACTTGTGGATTACAAGA  
ACCTCATTCTGTTGGATCTGGCAACAATAACATCGCTACTGTAGAGAACAAACACTTCAAG  
AACCTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCC  
GAAATTGCGGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA  
TCCTCCGGCACTTCAATGCCATGCCAAACTGAGGATCCTCATTCTCAACAACAAACCTG  
CTGAGGTCCCTGCCTGTGGACGTGTTGCTGGGTCTCGCTCTAAACTCAGCCTGCACAA  
CAATTACTCATGTACCTCCGGTGGCAGGGGTGCTGGACCAGTTAACCTCCATCATCC  
TAGACCTCCACGGAAACCCCTGGAGTGCTCTGCACAATTGTGCCCTTCAAGCAGTGGCA  
GAACGCTTGGGTTCCGAAGTGTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTT  
TAGAAAGGATTTCATGCTCCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT  
CGCCCACGTTAACCTCGCACAGTAAAACAGCACTGGGTGGCGGAGACCGGGACGCACTCC  
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTCGGTGTTGGTCCGGACTGCTGCTGG  
GTTTGTACCTCCGCCCTCACCGTGGGGCATGCTCGTGTATCCTGAGGAACCGAAAGC  
GGTCCAAGAGACGAGATGCCAACTCCTCCGCGTCCGAGATTAATTCCCTACAGACAGTCTGT  
GAECTTCTACTGGCACAATGGCCTTACAACGAGATGGGCCACAGAGTGTATGACTG  
TGGCTCTCACTCGCTCAGACTAACGACCCCAACCCCAATAGGGAGGGCAGAGGGAAAGGCG  
ATACATCCTCCCCACCGCAGGCACCCCGGGGCTGGAGGGCGTGTACCCAAATCCCC  
CCATCAGCCTGGATGGGCATAAGTAGATAAAACTGTGAGCTCGCACAACCGAAAGGGCCT  
GACCCCTACTTAGCTCCCTCCTGAAACAAAGAGCAGACTGTGGAGAGCTGGAGAGCGCA  
GCCAGCTCGCTTTGCTGAGAGCCCCTTGACAGAAAGCCAGCACGACCCCTGCTGGAG  
AACTGACAGTGCCCTGCCCTGGCCCCGGGCTGTGGGGTTGGATGCCGGTTCTATAC  
ATATATACATATCCACATCTATATAGAGAGATAGATATCTATTTCCTGTGGATTAG  
CCCCGTGATGGCTCCCTGTTGGCTACGCAAGGATGGCAGTTGCACGAAGGCATGAATGTAT  
TGTAAATAAGTAACCTTGACTTCTGAC

## FIGURE 34

MLLWILLLETSLCFAAGNVTGVCKEKICSCNEIEGDLHVDCEKKGFTSLQRFTA  
PTSQFYHLFLHGNSLTRLFPNEFANFYNAVSLHMENNGLHEIVPGAFGLQLVKRLH  
INNNKIKSFRKQTFGLDDLEYLQADFNLLRIDPGAFQDLNKLEVILILNDNL  
LISTLPANVFQYVPITHLDLRGNRLKTLPYEEVLEQIPGIAEILLEDPWDCTCD  
LLSLKEWLENIPKNALIGRVVCEAPTRLQGKDLNETTEQDLCPLKNRVDSSLP  
PAPPAQEETFAPGPLPTPFKTNGQEDHATPGSAPNGGTKI PGNWQIKIRPT  
AAIATGSSRNKPLANSLPCPGGCSDHIPGSGLKMNCNNRNVSSLADLKPKLS  
NVQELFLRDNKIHISRKSHFVDYKNLILLDLGNNNIATVENNTFKNLLDLRW  
LYMDSNYLDTLSREKFAGLQNLEYLNVEYNIAIQLILPGTFNAMPKLRLIL  
LNNNLLRSLPVDFAGVSLSKLSLHNNYFMYLPVAGVLDQLTSIIQIDLH  
GNPWECSCTIVPKQWAERLGSEVLMSDLKCETPVNFFRKDFM  
LLSND EICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVL  
VPGLLLVFVTS AFTVVGMLV FILRNRKRSKRRDANS SASEINSLQTV  
CDSSYWHNGPYNADGAHRVYDCGSHSLSD

**Signal sequence:**

amino acids 1-15

**Transmembrane domain:**

amino acids 618-638

**N-glycosylation site.**

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 122-126, 646-650

**Casein kinase II phosphorylation site.**

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,  
608-612, 657-661, 666-670, 693-697

**N-myristoylation site.**

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,  
354-360, 465-471, 493-499, 598-604, 603-609

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 337-348

## **FIGURE 35**

AGTCGACTCGTCCCCGTACCCGGGCCAGCTGTGTTCTGACCCCCAGAATAACTCAGGGC  
TGCACCGGGCCTGGCAGCGCTCCGCACACATTCTCTGCGGCCCTAACGGAAACTGTTGGC  
CGCTGGGCCCGGGGGGATTCTTGGCAGTTGGGGGTCCGTGGAGCGAGGGCGGAGGGG  
AAGGGAGGGGGAACCGGGTTGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC  
AGCTCTGCGTCCTCGAGCGGGACAGATCCAAGTGGGAGCAGCTCTCGTGCCTGGGGCCTCAG  
**AGAATGAGGCCGGCGTTGCCCTGTGCCTCTGGCAGGCCTCTGGCCCTGGGGCCTGCTACAGCCTGC**  
CGGCGAACACCCCAC TGCGACC GTGCTGGCTCGGCCTCGGGGGCCTGCTACAGCCTGC  
ACCACGCTACCATGAAGCGGCAGCGGCCGAGGAGGCCTGCATCCTGCGAGGTGGGGCGCTC  
AGCACCGTGCCTGCGGGCGCCGAGCTGCGCCTGTGCTCGCCTCTGCGGGCAGGCCAGG  
GCCCGGAGGGGGCTCAAAGACCTGCTGTTCTGGGTGCACTGGAGCGCAGGCGTTCCACT  
GCACCCCTGGAGAACGAGCCTTGCGGGGTTCTCTGGCTGTCCTCCGACCCCGGCGGTCTC  
GAAAGCGACACGCTGAGTGGGAGGCCAACGCTCCTGCACCGCGGGAGATGCGC  
GGTACTCCAGGCCACCGGTGGGGTCGAGGCCGAGGCTGGAAGGAGATGCGATGCCACCTGC  
GCGCCAACGGTACCTGTGCAAGTACCAAGTTGAGGTCTGTGTCCTGCGCCGCCCCGGG  
GCCGCCTCTAATTGAGCTATCGCGCCCTTCAGCTGCACAGCGCGCTCTGGACTTCAG  
TCCACCTGGGACCGAGGTGAGTGCCTGCGCTCGCGGGACAGCTCCCGATCTCAGTTACTGCA  
TCGCGGACGAAATCGCGCTCGCTGGACAAACTCTCGGGCGATGTGTTGTGTCCTGCCCC  
GGGAGGGTACCTCCGTGGCAAATGCGCAGAGCTCCCTAACTGCTTAGACGACTTGGGAGG  
CTTTCGCTGCAATGTGCTACGGGCTTCGAGCTGGGAAGGACGGCGCTTTGTGACCA  
GTGGGGAGGACAGCCGACCCCTGGGGGACCGGGGTGCCACCAGGCGCCGCCACT  
GCAACCAGCCCCGTGCCGAGAGAACATGGCAATCAGGGTCGACGAGAACGACTGGGAGAGAC  
ACCACCTGTCCCTGAACAAGACAATTCAAGTAACATCTATTCTGAGATTCTCGATGGGAT  
CACAGAGCACGATGTCTACCCCTCAAATGTCCTCAAGCCGAGTCAAAGGCCACTATCACC  
CCATCAGGGAGCGTGATTCCAAGTTAATTCTACGACTCCCTGCCACTCCTCAGGCTTT  
CGACTCCTCCCTGCCGTGGTCTTCATATTGTGAGCACAGCAGTAGTAGTGTGATCT  
TGACCATGACAGTACTGGGCTTGTCAAGCTCTGCTTCAAGAAAGCCCTTTCCAGCCA  
AGGAAGGAGTCTATGGGCCGCCGGCTGGAGAGTGTGATCTGAGCCGCTGCTTGGGCTC  
CAGTTCTGCACATTGCACAAACAATGGGTGAAAGTCGGGACTGTGATCTGCCAGAG  
CAGAGGGTGCCTTGCGGGAGTCCCTCTGGCTCTAGTGATGCAT**AGGGAAACAGGGGA**  
CATGGGCACTCCTGTGAACAGTTTCACTTTGATGAAACGGGAACCAAGAGGAACCTAC  
TTGTGTAAGTACAATTCTGCAGAAATCCCCCTCCTCTAAATTCCCTTACTCCACTGAG  
GAGCTAAATCAGAACTGCACACTCCTCCCTGATGATAGAGGAAGTGGAAAGTGCCTTAGGA  
TGGTGTACTGGGGACGGGTAGTGCTGGGAGAGATATTCTATGTTATTGGAGAA  
TTTGGAGAAGTGTGATTGAACTTTCAAGACATTGAAACAAATAGAACACAATATAATTACA  
TTAAAAAATAATTCTACCAAAATGGAAAGGAAATGTTCTATGTTAGGCTAGGAGTAT  
ATTGGTTGAAATCCCAGGGAAAAAATAAAAATTAAAGGATTGTTGAT

## **FIGURE 36**

MRPAFALCLLWQALWPAGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEACILRGGALS  
TVRAGAELRAVLALLRAGPGPGGGSKDLLFWVALERRSHTLENEPLRGFSWLSSDPGGL  
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCAPRPG  
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG  
RYLRAGKCAELPNCLDDLGFFACECATGFELGKDGRSCVTSGEGQPTLGGTGVPTRRPPATA  
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP  
SGSVISKFNSTTSSATPQAFDSSSAVVIFVSTAVVVLVILMTVLGLVKLCFHESPSSQPR  
KESMGPPGLESDPPEAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 399-418

**N-glycosylation site.**

amino acids 189-193, 381-385

**Glycosaminoglycan attachment site.**

amino acids 289-293

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 98-102, 434-438

**Casein kinase II phosphorylation site.**

amino acids 275-279, 288-292, 342-346, 445-449

**N-myristoylation site.**

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,  
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,  
477-483

**Aspartic acid and asparagine hydroxylation site.**

amino acids 262-274

## **FIGURE 37**

CGGACGGCTGGGATTCAAGCAGTGGCTGTGGCTGCCAGAGCAGCTCCTCAGGGAAACTAAG  
CGTCGAGTCAGACGGCACCATATCGCCTTAAAAGTGCCTCCGCCCTGCCGGCCCGTATC  
CCCCGGCTACCTGGGCCGCCCGCGCGGTGCGCGTGAAGAGGGAGCGCGCGGGCAGCGA  
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGGCCGTGTGAGCGCGTGGGTGCGGA  
GGGGCGTGTGCGCGCGCGCGTGGGTGCAAACCCGAGCGTCTACGCTGCCATGA  
GGGGCGCGAACGCCTGGCGCCACTCTGCCTGCTGGCTGCCGCCACCCAGCTCTCGCG  
CAGCAGTCCCCAGAGAGACCTGTTTACATGTGGTGGCATTCTACTGGAGAGTCTGGATT  
TATTGGCAGTGAAGGTTTCTGGAGTGTACCCCTCCAAATAGCAAATGTACTTGGAAAATCA  
CAGTTCCCAGGAAAAGTAGTCGTTCTCAATTCCGATTCAAGACCTCGAGAGTGACAAC  
CTGTGCCGCTATGACTTGTGGATGTGTACAATGCCATGCCATGGCCAGCGCATTGGCG  
CTTCTGTGGCACTTCCGGCTGGAGCCCTGTGTCCAGTGGCAACAAGATGATGGTGCAGA  
TGATTCTGATGCCAACACAGCTGGCAATGGCTCATGGCCATGTTCTCCGCTGCTGAACCA  
AACGAAAGAGGGATCAGTATTGTGGAGGACTCCTGACAGACCTCCGGCTTTAAAAC  
CCCCAACTGGCCAGACGGGATTACCTGCAGGAGTCACCTGTGTGGCACATTGTAGCCC  
CAAAGAATCAGTTAGAATTAAAGTTGAGAAGTTGATGTGGAGCGAGATAACTACTGC  
CGATATGATTATGTGGCTGTGTTAATGGCGGGAAAGTCAACGATGCTAGAAGAATTGGAAA  
GTATTGTGGTGTAGTCCACCTGCGCCAATTGTGCTGAGAGAAATGAACTTCTTATTCACT  
TTTATCAGACTTAAGTTAAC TGCAAGATGGTTATTGGTCACTACATATTCAAGGCCAAA  
AAACTGCCTACAACACAGAACAGCCTGTCACCACCATTCCTGTAACCACGGTTAAA  
ACCCACCGTGGCCTTGTGTCACAAAAGTGTAGACGGACGGGACTCTGGAGGGCAATTATT  
GTTCAAGTGACTTGTATTAGCCGGACTGTTACACACCACACTCGCGATGGGAGTTG  
CACGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTGGCGATT CAGCAGGCC  
CAAGAACATGAGTGCCAGGCTGACTGTCGCTGCAAGCAGTGCCCTCTCCTCAGAAGAGGTC  
TAAATTACATTATTATGGCCAAGTAGGTGAAGATGGCGAGGCAAATCATGCCAACAGC  
TTTATCATGATGTTCAAGACCAAGAACATCAGAACGCTCCTGGATGCCCTAAAAAATAAGCAATG  
TTAACAGTGAACGTGTCATTAAAGCTGTATTCTGCCATTGCCCTTGAAAGATCTATGTC  
TCTCAGTAGAAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG  
GACTGGTTGACTCTTCACATGATGGAGGTATGAGGCCTCCGAGATAGCTGAGGGAAAGTTCTT  
TGCCCTGCTGTCAGAGGAGCAGCTATCTGATTGGAAACCTGCCGACTTAGTGCCTGATAGGA  
AGCTAAAAGTGTCAAGCGTTGACAGCTTGGAAAGCGTTATTATACATCTGTAAAAGGAT  
ATTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAAGATT TAGAAGTGCATATTATAGT  
GTTATTTGTTCACCTCAAGCCTTGCCCTGAGGTGTTACAATCTGTCTGCGTTCTA  
AATCAATGCTAATAAAATATTAAAGGAAAAAAAAAAAAA

## **FIGURE 38**

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESGFIGSEGFPGVYPPNSKCTWK  
ITVPEGKVVVLNFRFIDLESDNLCRYDFDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV  
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLDRPSGSFKTPNWPDYDYPAGVTCVWHIV  
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGEVNDARRIGKYCGDSPPAPIVSERNELLI  
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTFPVTTGLKPTVALCQQKCRRTGTLEGN  
YCSSDFVLAGTVITTITRD GSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR  
GLNYIIMGQVGEDGRGKIMPNSFIMMF KTKNQKL DALKNKQC

**Signal sequence:**

amino acids 1-23

**N-glycosylation site.**

amino acids 355-359

**Casein kinase II phosphorylation site.**

amino acids 64-68, 142-146, 274-278

**Tyrosine kinase phosphorylation site.**

amino acids 199-208

**N-myristoylation site.**

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,  
305-311, 309-315, 320-326, 330-336

**Cell attachment sequence.**

amino acids 149-152

## **FIGURE 39**

CGGACCGCGTGGCGGGACCGCGTGGCGGCCACGGCGCCCGGGCTGGGCGGTGCCTTCTT  
CCTTCTCCGTGGCTACGAGGGTCCCCAGCCTGGTAAAGATGGCCCCATGGCCCCGAAGG  
GCCTAGTCCCAGCTGTGCTCTGGGCCTCAGCCTCTTCACACCTCCAGGACCTATCTGG  
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCGCCTCAGCCCCATCCGTGTACACCTG  
CCGGGGACTGGTTGACAGCTTAACAAGGGCCTGGAGAGAACCATCCGGACAACTTGGAG  
GTGGAAACACTGCCTGGGAGGAAGAGAATTGTCAAATACAAAGACAGTGAGACCCGCCTG  
GTAGAGGTGCTGGAGGGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCT  
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTACAAGCAGCAGGAGGCCGGACCTCTCC  
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTCGGGCCCTCCTGC  
CTTCCCTGTCTGGGAAACAGAGAGGCCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAAGG  
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGTACGGGGTGAGGCCTGTGGCC  
AGTGTGGCCTGGCTACTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTGGCTTGT  
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACGTGGCAATGCAAGAAGGG  
CTGGGCCCTGCATCACCTCAAGTGTAGACATTGATGAGTGAGCAGAGGCCAACT  
GTGGAGCTGACCAATTCTCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG  
GCCTGCCTAGGCTGCATGGGGCAGGGCCAGGTCGCTGTAAGAAGTGTAGCCCTGGCTATCA  
GCAGGTGGCTCCAAGTGTCTCGATGGATGAGTGTGAGACAGAGGTGTCCGGAGAGA  
ACAAGCAGTGTAAAACACCGAGGGCGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG  
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTCAGAGATGAC  
AGAAGACGAGTTGGTGGTGCTGCAGCAGATGTTCTTGGCATCATCATCTGTGCACTGGCCA  
CGCTGGCTGCTAAGGGCAGTTGGTGTACCGCCATCTCATTGGGCTGTGGCGGCCATG  
ACTGGCTACTGGTTGTCAAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATA  
ATCGCGGCCACCACCTGTAGGACCTCCCACCCACGCTGCCCGAGAGCTTGGCTGCC  
TCCTGCTGGACACTCAGGACAGCTTGGTTATTTTGAGAGTGGGTAAGCACCCCTACCTG  
CCTTACAGAGCAGCCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTAAAAGTAGC  
CCTGAAGGTGGATACCATGAGCTTCACTGGGGACTGGCAGGCTTCACAATGTGTGA  
ATTTCAAAAGTTTCTTAATGGTGGCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTG  
GTCCTCACAGGGTGGGCCATCACAGCTCCCTGCCAGCTGCATGCCAGTTCTGT  
TCTGTGTTACCCACATCCCCACACCCATTGCCACTTATTATTCATCTCAGGAAATAAGA  
AAGGTCTTGGAAAGTTAAAAAAAAAAAAAAA

## **FIGURE 40**

MAPWPPKGVLPAVLWGLSLFLNLPGPIWLQPSPPPQQSSPPQPHPCHTCRGLVDSFNKGLER  
TIRDNFGGGNTAWEEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLESELVESWWFHKQ  
QEAPDLFQWLCSDSLKLCCPAGTFGPSCLPCCPGGTERPCGGYGCCEGEGTRGGSGHCDCQAG  
YGGECACGQCGLGYFEAERNASHLVCACFGPCARCSGPEESNLQCKKGWALHHLKCVDIDE  
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKCSPGYQQVGSKCLDVDECE  
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLQQMFFG  
IIICALATLAKGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

**Signal sequence:**

amino acids 1-29

**Transmembrane domain:**

amino acids 372-395

**N-glycosylation site.**

amino acids 79-83, 205-209

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 290-294

**Casein kinase II phosphorylation site.**

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

**N-myristoylation site.**

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,  
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,  
326-332, 372-378, 395-401

**Aspartic acid and asparagine hydroxylation site.**

amino acids 321-333

**EGF-like domain cysteine pattern signature.**

amino acids 181-193

## **FIGURE 41**

TGAGACCCTCCTGCAGCCTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCCTCCAGGGCA  
GCACCATGCCAGCCCCTGTGGCTCTGCTGGGACTCTGGGTGTTGCCCTGCCAGCCCCGGG  
GCCGCCCTGACCGGGGAGCAGCTCCTGGCAGCCTGCTGCCAGCTGCAGCTCAAAGAGGT  
GCCCACCCCTGGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCAGT  
ACGTGGCCCTGCTGCAGCGCAGCCACGGGACCGCTCCCGCGAAAGAGGTTCAGCCAGAGC  
TTCCGAGAGGTGGCCGGCAGGTTCCCTGGCGTTGGAGGCCAGCACACACCTGCTGGTGGTCGG  
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTCAGGCCGTGCTGCCGTCTTCAGG  
AGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGGCGGCTGTCCCCGCGCAGGCCGGGCC  
CGGGTACCGTCGAGTGGCTGCCGTCCCGACGACGGCTCCAACCGCACCTCCCTCATCGA  
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCTTCGACGTGACCGAGGCCGTGA  
ACTTCTGGCAGCAGCTGAGCCGGCCCCGGCAGCCGCTGCTGCTACAGGTGTCGGTGCAGAGG  
GAGCATCTGGCCCGCTGGCGTCCGGCCACAAGCTGGTCCGCTTGCCCTCGCAGGGGGC  
GCCAGCCGGCTTGGGAGCCCCAGCTGGAGCTGCACACCCCTGGACCTTGGGACTATGGAG  
CTCAGGGCAGCTGTGACCCCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG  
ATGTACATTGACCTGCAGGGATGAAGTGGGCGAGAACTGGGTGCTGGAGGCCCGGGCTT  
CCTGGCTTATGAGTGTGGCACCTGCCGGCAGCCCCGGAGGCCCTGGCCTTAAGTGGC  
CGTTCTGGGCCTCGACAGTCATGCCCTGGAGACTGACTCGCTGCCATGATCGTCAGC  
ATCAAGGAGGGAGGCAGGACCAGGCCAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA  
GTGCAGCTGTGCCTCGATGGTGCCTCGTGCCTAGGCCAAGGAGGCTCCAGCCATAGGGCCTAGTG  
TAGCCATCGAGGGACTTGACTTGTGTGTTCTGAAGTGGTGCAGGGTACAGGAGAGCTG  
GCGATGACTGAAGTGCCTGATGGACAAATGCTCTGTGCTCTAGTGAGCCCTGAATTGCTT  
CCTCTGACAAGTTACCTCACCTAATTTGCTCTCAGGAATGAGAATCTTGGCCACTGGA  
GAGCCCTGCTCAGTTCTCTATTCTATTCACTGCACTATATTCTAACACTTACAT  
GTGGAGATACTGTAACCTGAGGGCAGAAAGGCCANTGTGTCATTGTTACTGTCCCTGTCAC  
TGGATCTGGCTAAAGTCCTCCACCACACTGGACCTAACAGACCTGGGTTAAGTGTGGGT  
TGTGCATCCCCAATCCAGATAATAAGACTTTGAAAACATGAATAAACACACATTATTCT  
AAAA

## **FIGURE 42**

MQPLWLCWALWVLPLASPGAAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV  
ALLQRSHGDRSRGKRFQSFRREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP  
VPKAALHRHGRLSPRSARARVTVEWLVRDDGSNRTSLIDSRLVSHESGWKAFDVTEAVNF  
WQQLSRPRQPLLQSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLGDYGAQ  
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWPF  
LGPRQCIASETDSLPMIVSIKEGGRTQPVVSLPNMRVQKCSCASDGALVPRRLQP

**Signal sequence:**

amino acids 1-18

**N-glycosylation site.**

amino acids 158-162

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 76-80

**Casein kinase II phosphorylation site.**

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

**N-myristoylation site.**

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

**Amidation site.**

amino acids 74-78

**TGF-beta family signature.**

amino acids 282-298

## **FIGURE 43**

GTCTGTTCCCAGGAGTCCTCGCGGCTGTTGTCACTGGCCTGATCGCGATGGGACAAA  
GGCGCAAGTCGAGAGGAAACTGTTGTGCCTCTCATATTGGCGATCCTGTTGTGCTCCCTGG  
CATTGGGCAGTGTACAGTCACCTGAACCTGAAGTCAGAATTCCCTGAGAATAATCCT  
GTGAAGTTGTCTGTGCCACTCGGGCTTTCTTCTCCCCGTGTGGAGTGGAAAGTTGACCA  
AGGAGACACCACCAGACTCGTTGCTATAATAACAAGATCACAGCTCCTATGAGGACCGGG  
TGACCTTCTTGCCAACGGTATCACCTCAAGTCCGTGACACGGGAAGACACTGGGACATAC  
ACTTGTATGGTCTCTGAGGAAGGCGAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT  
GCTTGTGCCCTCATCCAAGCCTACAGTTAACATCCCTCCTGCCACCATTGGGAACCGGG  
CAGTGCTGACATGCTCAGAACAGATGGTCCCCACCTTCTGAATAACACACTGGTTCAAAGAT  
GGGATAGTGTGCTACGAATCCAAAAGCACCCGTGCCCTCAGCAACTCTCCTATGTCCT  
GAATCCCACAAACAGGAGAGCTGGTCTTGATCCCTGTCAAGCTCTGATAACTGGAGAATACA  
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTCAAATGCTGTGCGCATGGAAAGCT  
GTGGAGCGGAATGTGGGGTCATCGTGGCAGCCGTCTTGTAAACCTGATTCTCCTGGGAAT  
CTTGGTTTTGGCATCTGGTTGCCTATAGCCGAGGCCACTTGACAGAACAAAGAAAGGGA  
CTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCGAAGTGAAGGAGAATTCAAACAG  
ACCTCGTCATTCTGGTGTGAGCCTGGTCGGCTACCGCCTATCATCTGCATTGCCTTACT  
CAGGTGCTACCGACTCTGGCCCTGATGTCAGTTCACAGGATGCCTTATTGTCCT  
TACACCCACAGGGCCCCCTACTTCTCGGATGTGTTTAATAATGTCAGCTATGTGCC  
ATCCTCCTCATGCCCTCCCTCCCTTACCACTGCTGAGTGGCTGGAACTTGTAA  
GTGTTATTCCCCATTCTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC  
TTCTAAGTAGACAGAAAAATGGGGGGTCGCAGGAATCTGCACTCAACTGCCACCTGGC  
TGGCAGGGATCTTGAATAGGTATCTTGAGCTGGTCTGGCTCTTCCCTGTACTGAC  
GACCAGGGCCAGCTGTTCTAGAGCGGGATTAGAGGCTAGAGCGGCTGAAATGGTTGG  
TGATGACACTGGGTCTTCCATCTCTGGGCCACTCTCTGCTTCCATGGAAAGTG  
CCACTGGGATCCCTGCCCCTGCTCTGAATACAAGCTGACTGACATTGACTGTCTGT  
GGAAAATGGGAGCTTGTGGAGAGCATAGTAAATTTCAGAGAACTTGAAGCCAAAAG  
GATTAAAACCGCTGCTCTAAAGAAAAGAAAATGGAGGCTGGCGCAGTGGCTCACGCC  
TAATCCCAGAGGCTGAGGCAGGCAGGATCACCTGAGGTGGAGTTGGGATCAGCCTGACCA  
ACATGGAGAAACCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC  
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAAACTCCAGCTCAAAAAAAAAAAAAA

## **FIGURE 44**

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPKLSCAYSGFSSPRVEW  
KFDQGDTTRILVCYNNKITASYEDRVTFLPTGITFKSVTREDTGYTCMVSEEGGNSYGEVKV  
KLIVLVPPSKPTVNI PSSATIGNRAVLTCSEQDGSPPSEYTWFKDGVMPNPKSTRAFSNS  
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLI  
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

**Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 238-255

**N-glycosylation site.**

amino acids 185-189

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 270-274

**Casein kinase II phosphorylation site.**

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,  
193-197, 203-207, 287-291

**N-myristoylation site.**

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

## **FIGURE 45**

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGAGCGCGTTGGATGGCGCAGGTTGGA  
GCGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT  
GGAGGCCGCGCGAGCCGCTTCCACCCGACCTCTGCCAGGCCAGGCCAGGCCCCAGCTCAG  
GCTCGTCCCACCCACCAAGTCCAGTGCCGACCAGTGGCTTATGCGTCCCCTCACCTGG  
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC  
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCTGCCCTGCACCGCGTCA  
GTGACTGCTCTGGGGAACTGACAAGAAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCA  
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCA  
CCCAGACTGTCCCAGCGACGAGCTGGCTGTGGAACCAATGAGATCCTCCCGGAAG  
GGGATGCCACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTACCTCTCAGGAATGCC  
ACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTCCCTCTGTGGGAATGCCACATCCTC  
CTCTGCCGGAGACCAGTCTGGAAGGCCAAGTGCCTATGGGTTATTGCAGCTGCTGCCGTGC  
TCAGTGCAAGCCTGGTCACGCCACCCCTCCTCCTTGTCCCTGGCTCCGAGCCCAGGAGCGC  
CTCCGCCACTGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGTCAGAACAGAAC  
CTCGCTGCCTGAGGACAAGCACTTGCCACCAACCGTCACTCAGCCCTGGCGTAGCCGGACA  
GGAGGAGAGCAGTGATGCGGATGGTACCCGGCACACCAGCCCTCAGAGACCTGAGTTCTT  
CTGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC  
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGAACCTGCCACAGCCAGAAC  
GGGCTGGCCCCAGGCAGCTCCAGGGGGTAGAACGCCCTGTGCTTAAGACACTCCCTGCTG  
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

## **FIGURE 46**

MSGGWMAQVGAWRTGALGLALLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR  
TSGLCVPLTWRCRDLDGSDEEECRIEPCTQKGQC PPPGLPCPCTGVSDCSGGDKKL  
RNC SRLA CLAGELRCTL SDDCIPLTWRC DGH PDCP DSS DEL GCGTNEILPEGDATTMGPV  
LESVTSLRNATTMGPVTL ES VPS VGNATSSAGDQSGSPTAYGVIAAAAVLSASLVTATLL  
LLSWLRAQERLRPLG LLLVAMKESLLLSEQKTSLP

**Signal sequence:**

amino acids 1-30

**Transmembrane domain:**

amino acids 230-246

**N-glycosylation site.**

amino acids 126-130, 195-199, 213-217

**Casein kinase II phosphorylation site.**

amino acids 84-88, 140-144, 161-165, 218-222

**N-myristoylation site.**

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,  
224-230, 230-236, 263-269

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 44-55

**Leucine zipper pattern.**

amino acids 17-39

## **FIGURE 47**

CCACCGCGTCGGTCTCGCTCGCGCAGCGGCCAGCAGAGGTCGCCACAGATGCCG  
GTTAGACTGGCGGGGGAGGAGGCGGAGGAGGAAGGAAGCTGCATGCATGAGACCCACAGA  
CTCTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTTATCATGGAATGAACCCGAGCAATG  
GAGATGGATTCTAGAGCAGCAGCAGCAGCACACCTCAGTCCCCCAGAGACTCTTG  
GCCGTGATCCTGTGGTTTAGCTGGCGCTGTGCTCGGCCCTGCACAGCTCACGGCGGGTT  
CGATGACCTCAAGTGTGCTGACCCCGCATTCCCGAGAATGGCTTCAGGACCCCCAGCG  
GAGGGGTTTCTTGAAAGGCTCTGTAGCCGATTTCACTGCCAAGACGGATTCAAGCTGAAG  
GGCGCTACAAAGAGACTGTGTTGAAGCATTAAATGGAACCTAGGCTGGATCCAAGTGA  
TAATTCCATCTGTGCAAGAAGATTGCCGTATCCCTCAAATGAAGATGCTGAGATTATA  
ACAAGACATATAGACATGGAGAGAACGTAATCATCACTTGTATGAAGGATTCAAGATCCGG  
TACCCGACCTACACAATATGGTTTCAATTATGTCGCGATGATGGAACGTGGAATAATCTGCC  
CATCTGTCAAGGCTGCCTGAGACCTCTAGCCTCTTAATGGCTATGTAAACATCTCTGAGC  
TCCAGACCTCCTCCCGTGGGACTGTGATCTCCTATCGCTGCTTCCGGATTAAACTT  
GATGGGTCTGCGTATCTTGAGTGTCTACAAAACCTTATCTGGCGTCCAGCCCACCCGGTG  
CCTTGCTCTGGAAGCCAAGTCTGTCCACTACCTCCAATGGTAGTCACGGAGATTCGTCT  
GCCACCCGCGCCTTGTGAGCGTACAACCACGGAACGTGGTGGAGTTTACTGCGATCCT  
GGCTACAGCCTCACCAAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCCCTC  
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCCTCTGA  
CCACGTGGAAGATTGTGGCGTTACGGCAACCAGTGTGCTGGTGTGCTCGTCATC  
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTCCCCCAGGGGCTCCCGGAG  
TTCCAGCAGTGACCTGACTTTGTGGTAGACGGCGTGCCTCATGCTCCGTCTATG  
ACGAAGCTGTGAGTGGCGCTTGAGTGCCTTAGGCCCGGGTACATGGCTCTGTGGCCAG  
GGCTGCCCTTACCGTGGACGACCAGAGCCCCCAGCATACCCGGCTCAGGGACACGGA  
CACAGGCCAGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTGAGCTGCTCCAAA  
GTCTGTATTCACCTCCAGGTGCCAAGAGAGCACCCACCTGCTGGACAACCTGACATA  
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCAGGCATCCATGCCCACGGT  
GTTGTTCTAAGAAACTGATTGATTAAAAAATTCCAAAGTGTCTGAAGTGTCTCTCAA  
ATACATGTTGATCTGTGGAGTTGATTCCCTTCTCTTGAGTGGTTAGACAAATGTAAACAA  
AGCTCTGATCTTAAAATTGCTATGCTGATAGAGTGGTAGGGCTGGAAGCTTGATCAAGTC  
CTGTTCTTCTTGACACAGACTGATTAAAATTAAAAGNAAAAAA

## **FIGURE 48**

MYHGMNPSNGDFLEQQQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI  
PENGFRTPSGGVFFEGSVARFHQCQDGFKLGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI  
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICGGCLRPLAS  
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLP  
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSODYITCQYGEWFPSYQVYCIKSEQT  
WPSTHETLLTWKIVAFATSVLLVLLVILARMFQTKFKAHFPPRGPPRSSSDPDFVVVD  
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGD'TDGPGESETCDS  
VSGSELLQSLYSPPRCQESTHPASDNPDIIASTAEEVASTSPGIHHAHWVLFLRN

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 325-344

**N-glycosylation site.**

amino acids 104-108, 134-138, 192-196

**Casein kinase II phosphorylation site.**

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,  
364-368, 380-384, 467-471, 468-472

**N-myristoylation site.**

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,  
478-484

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 394-405

## **FIGURE 49**

CCACCGCGTCCGCTCCGCCTCCCCCGCCTCCCGTCGGTCCGTGGCCTAGAGA  
TGCTGCTGCCCGGGTTGCAGTTGTCGCGCACGCCCTGCCGCCAGCCGCTCCACCGCCGT  
AGCGCCCGAGTGTGGGGGGCGCACCCGAGTCGGGCCATGAGGCCGGAACCGCGCTACAGG  
CCGTGCTGCTGCCGTGCTGGTGGGCTGCCGCCAGGGTCGCCTGCTGAGTGCC  
TCGGATTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCCTGTTA  
TAAAGTCATTACTTCCATGATACTTCTGAAGACTGAACCTTGAGGAAGCAAAGAACCT  
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA  
AAGTCATTGAAAACCTCTGCCATCTGATGGTACCTCTGGATTGGCTCAGGAGGCCTGA  
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTATGCTTGGACTGATGGCAGCATAT  
CACAACTTAGAACCTGGTATGTGGATGAGCCGTCCGCCAGCGAGGTCTGCGTGGTCATG  
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAAATGATGA  
CCGGTGCAACATGAAGAACAAATTTCATTGCAAATATTCTGATGAGAAACCAGCAGTCCTT  
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAAACACAG  
GAAGAACATGCCAAAAAAACATTAAAGAAAGTAGAGAACAGCTGCCTGAATCTGGCCTACAT  
CCTAATCCCCAGCATTCCCCTCTCCTCCTGTGGTACCCACAGTTGTATGTTGGGTTT  
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCCCTAGCACAAAGAACACACCATC  
TGGCCTCTCCTCACCAAGGAAACAGCCGGACCTAGAGGTCTACAATGTATAAGAAAACA  
AAGCGAAGCTGACTTAGCTGAGACCCGCCAGACCTGAAGAATATTCAATTCCGAGTGTGTT  
CGGGAGAAGCCACTCCGATGACATGTCTGTGACTATGACAACATGGCTGTGAACCCATCA  
GAAAGTGGTTGTGACTCTGGTGGAGAGTGGATTGTGACCAATGACATTATGA  
GTTCTCCCCAGACCAAATGGGAGGAGTAAGGAGTCTGGATGGGTGAAAATGAAATATATG  
GTTATTAGGACATATAAAAACTGAAACTGACAACAAATGGAAAAGAAATGATAAGCAAAATC  
CTCTTATTTCTATAAGGAAAATACACAGAACGGTCTATGAACAAGCTTAGATCAGGTCTGT  
GGATGAGCATGTGGTCCCCACGACCTCCTGTGGACCCCCACGTTGGCTGTATCCTTTAT  
CCCAGCCAGTCATCCAGCTCGACCTTATGAGAACGGTACCTGCCAGGTCTGGCACATAGTA  
GAGTCTCAATAATGTCACTTGGTTGGTGTATCTAACTTTAAGGGACAGAGCTTACCTG  
GCAGTGATAAAAGATGGGCTGTGGAGCTTGGAAAACCACCTCTGTTCTGCTATACAG  
CAGCACATATTATCATAACAGACAGAAAATCCAGAACATCTTCAAAGCCCACATGGTAGCACAG  
GTTGGCCTGTGCATCGCAATTCTCATATCTGTTTTCAAAGAATAAAATCAAATAAAGA  
GCAGGAAAAAAA

## **FIGURE 50**

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRGGQPVCRGGTQRPCYKVIYFHDTSRRL  
NFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFWIGLRRREEQSNSTACQDL  
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNFICKY  
SDEKPAVPSREAEGEETELTPVLPETQEEDAKKTFKESREAALNLAYILIPSIPLLLL  
VTTVVVCWWICRKRKREQPDPSKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL  
KNISFRVCSGEATPDDMSCDYDNMAVNPSSEGFTLVSVESGFVTNDIYEFSPDQMGRSKES  
GWVENEIYGY

**Signal sequence:**

amino acids 1-21

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site.**

amino acids 117-121, 312-316

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 296-300

**Casein kinase II phosphorylation site.**

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,  
299-303, 306-310, 323-327

**N-myristoylation site.**

amino acids 18-24, 37-43, 76-82, 146-152

## **FIGURE 51**

GGGGTCTCCCTCAGGCCGGGAGGCACAGCGTCCCTGCTGAAGGGCTGGATGTACGC  
ATCCGCAGGTTCCCGCGGACTTGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT  
GTTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGT  
GTTCAGCATGCGCTTGTGGACCCCAGTGGCGTCTGACCTCGCTGGCGTACTGCCTGCACC  
AGCGCGGGTGGCCCTGGCGAGCTGCAGGAGGCCATGCCAGTGTCCGGTCACCGCAGC  
CTGCTGAAGTTGAAAATGGTGCAGGTGTTGACACGGGGCTGGAGTCCCTCAAGCC  
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCAAACTC  
AGTTGATTACACAGTCACCAATCTAGCTGGTGTCCGAAACCATAATTCTCCTTACGACTCT  
CAATACCATGAGACCACCCCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCAT  
GCAGCAAATGTTGCCTGGAGAGAGACTGAGGAAGAACTATGTGAAGACATTCCCTTC  
TTTCACCAACCTCAACCCACAGGAGGTCTTATTGTTCCACTAACATTTCGGAATCTG  
GAGTCCACCCGTTGTTGCTGGCTGGCTTTCCAGTGTCAAGAAAGAAGGACCCATCATCAT  
CCACACTGATGAAGCAGATTCAAAGTCTGTATCCAACTACCAAAGCTGGAGCCTGA  
GGCAGAGAACCAAGAGGCCGGAGGCAGACTGCCTCTTACAGCCAGGAATCTCAGAGGATTG  
AAAAAGGTGAAGGACAGGATGGCATTGACAGTAGTGTATAAGTGGACTTCTCATCCTCCT  
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCAAGCTGCCCATGCTGAAGAGATTG  
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTGTACATACTGCCAAGGAAGACAGG  
GAAAGTCTTCAGATGGCAGTAGGCCATTCCCTCACATCCTAGAGAGCAACCTGCTGAAAGC  
CATGGACTCTGCCACTGCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATG  
TGACCTTCATACCGCTTTAATGACCTGGGGATTTTGACCACAAATGCCACCGTTGCT  
GTTGACCTGACCATGGAACCTTACCAAGCACCTGGAATCTAAGGAGTGGTTGTGCAGCTCTA  
TTACCAACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCCGCTGGACATGT  
TCTTGAATGCCATGTCAGTTACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA  
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTACTGATTATAAAAGCAGGATGTGTTGATT  
TTAAAATAAAAGTGCCTTATACAATG

## **FIGURE 52**

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELOEADGQCPVDRSLLKLKMVQVVFRHGAR  
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL  
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNQEVFIRSTNIFRNLESTRCLLAGLFQCQKE  
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTASLQPGISEDLKKVKDRMGIDSSDKVD  
FFILLDNVAAEQAHNLPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFLHILES  
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW  
FVQLYYHGKEQVPRGCPDGLCP LDMLNAMS VYTLSPEKYHALCSQTQVM EVGNEE

**Signal sequence:**

amino acids 1-23

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 218-222

**Casein kinase II phosphorylation site.**

amino acids 87-91, 104-108, 320-324

**Tyrosine kinase phosphorylation site.**

amino acids 280-288

**N-myristoylation site.**

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

**Amidation site.**

amino acids 216-220

**Leucine zipper pattern.**

amino acids 10-32

**Histidine acid phosphatases phosphohistidine signature.**

amino acids 50-65

## **FIGURE 53**

CTCCTCTAACATACTTGCAGCTAAACTAAATATTGCTGCTGGGGACCTCCTTAGCCT  
TAAATTCAGCTCATCACCTCACCTGCCTGGTCATGGCTCTGCTATTCTCCTTGATCCTT  
GCCATTGACCAGACCTGGATTCCCTAGCGTCTCCATCTGGAGTGC GGCTGGTGGGGGCCT  
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGACCGTGTGATG  
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGTGCCGGAGCTGGCTGTGGAGCTGCCAGC  
GGAACCCCTAGTGGTATTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCTCATCCA  
ATCAGTCAGTTGCACAGGAACAGAAGATACTGGCTCAGTGTGAGCAAGAAGAAGTTATG  
ATTGTTCACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGCTCTTCTCCCCA  
GTCCCAGAGGGTGTCAAGGCTGGTGACGCCCTGGCATTGCAAGGGACGCGTGGAAAGTGAA  
GCACCAAGAACCAAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGCCGCAAAGGTGG  
TGTGCCGGCAGCTGGATGTGGGAGGGCTGTACTGACTCAAAAACGCTGCAACAAGCATGCC  
TATGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCTTCA  
GGATTGCCCTCTGGCCTGGGGAAAGAACACACCTGCAACCAGATGAAGACACGTGGTCG  
AATGTGAAGATCCCTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGCGACTG  
GAGGTGCTGACAAGGGGTATGGGCTCTGTCTGTGATGACAACACTGGGAGAAAAGGAGGA  
CCAGGGTGTATGCAAGCAACTGGCTGTGGAAAGTCCCTCTCCCTCAGAGACCGGA  
AATGCTATGCCCTGGGGTTGCCGATCTGGCTGGATAATGTTGCTCAGAGGAGGAG  
CAGTCCCTGGAGCAGTGCCAGCACAGATTTGGGGTTCACGACTGCACCCACCAGGAAGA  
TGTGGCTGTCATCTGCTCAGTGTAGGTGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA  
GAAAAACACAGAAGAAGGGAGCATTACTGTCTACATGACTGCATGGATGAACACTGATCT  
TCTTCTGCCCTGGACTGGACTTATACTTGGTGCCCTGATTCTCAGGCCTTCAGAGTTGG  
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTGGAACACTACATCA  
CCACCTTCCTATGTCTCCACATTGCACACAGCAGATTCCAGCCTCCATAATTGTGTGTAT  
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACACACATA  
CACCAATTGTCCTGTTCTCTGAAGAACTCTGACAAAATACAGATTTGGTACTGAAAGAGA  
TTCTAGAGGAACGGAATTAAAGGATAAATTCTGAATTGGTATGGGTTCTGAAATTG  
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACCTTATTACAATAATAAGATAGCAC  
TATGTGTTCAAA

## **FIGURE 54**

MALLFSLILAICTRPGLASPSGVRLVGGHLRCEGRVEVEQKGQWGTVCDDGWDIKDVAVL  
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC  
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVCQTGWSLRAAKVVCRQLGCGRAVL  
TQKRCNKHAYGRKPIWLSQMCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG  
GDNLCGSRLEVLLHKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIDL  
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

**Signal sequence:**

amino acids 1-15

**Casein kinase II phosphorylation site.**

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,  
267-271, 294-298, 316-320, 336-340

**N-myristoylation site.**

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,  
180-186, 263-269, 286-292

**Amidation site.**

amino acids 196-200

**Speract receptor repeated domain signature.**

amino acids 29-67, 249-287

## **FIGURE 55**

ACTGCACTCGGTCTATCGATTGAATTCCCCGGGATCCTCTAGAGATCCCTCGACCTCGAC  
CCACCGGTCCCGGGACCGTGGCGGACCGTGGCGGCTACCAGGAAGAGTCTGCCGAAG  
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCCCTGCTGTTGGCTGCCTGGG  
CGTCTTCGGCCTTTCCGGCTGCTGCAGTGGGTGCGCGGGAAAGGCCTACCTGCGGAATGCTG  
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGCAAAGAATGTGCAAAAGTCTTCTATGCT  
GCGGGTGCTAAACTGGTGCTCTGTGGCCGAATGGTGGGCCCTAGAACAGCTCATCAGAGA  
ACTTACCGCTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC  
TCACAGACTCTGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTGGCTATGTC  
GACATACTTGTCAACAATGCTGGATCAGCTACCGTGGTACCATCATGGACACACCACAGTGG  
TGTGGACAAGAGGGTCATGGAGACAAACTACTTGGCCCAGTTGCTCTAACGAAAGCACTCC  
TGCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG  
ATGAGCATTCCCTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTGA  
CTGTCGCGTCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA  
TCCACACCAACCTCTGTAAATGCCATCACCGCGGATGGATCTAGGTATGGAGTTATGGAC  
ACCACCCACAGCCCAGGGCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTGCTGCTGTGGG  
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCCTGGCTGTTATCTCGAA  
CTCTGGCTCCTGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC  
AAGAACTCCTAGTACTCTGACCAGCCAGGGCAGAGAACAGCAGCACTTTAGGCTTGC  
TTACTCTACAAGGGACAGTTGCATTGAGACTTAATGGAGATTGCTCACAAGTGG  
AAAGACTGAAGAACACATCTCGTCAGATCTGCTGGCAGAGGACAATAAAAACGACAACA  
AGCTTCTCCAGGGTGAGGGAAACACTTAAGGAATAATGGAGCTGGGTTAACACT  
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAGGGCGGCCGACTCTAG  
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCAATTGTTATTGCAGCTTATAATGGTTAC

## **FIGURE 56**

MDFITSTAILPLLGCLGVFGLFRLLQWVRGKAYLRNAVVIITGATSGLGKECAKVFYAAGA  
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAEILQCFGYVDIL  
VNNAGISYRGTIMDTTVVDKRVMETNYFGPVALTKALLPSMIKRQQGHIVAISSIQGKMSI  
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT  
AQGRSPVEVAQDVLAAVGKKKDVLADLLPSLAVYLRTLAPGLFFSLMASRARKERKSNS

**Signal sequence:**

amino acids 1-21

**Transmembrane domain:**

amino acids 104-120, 278-292

**N-glycosylation site.**

amino acids 228-232

**Glycosaminoglycan attachment site.**

amino acids 47-51

**Casein kinase II phosphorylation site.**

amino acids 135-139, 139-143, 253-257

**Tyrosine kinase phosphorylation site.**

amino acids 145-153, 146-153

**N-myristoylation site.**

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

**Amidation site.**

amino acids 265-269

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 6-17

## **FIGURE 57**

## **FIGURE 58**

MKFLLDILLPLLIIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK  
LVLWDINKHGLEETAAKCKGLGAKVHTFVVDCSNREDIYSSAKVKAEIGDVSILVNNAGVV  
YTSDFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLAYC  
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH  
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

**Signal sequence:**

amino acids 1-19

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-34, 283-287

**Casein kinase II phosphorylation site.**

amino acids 52-56, 95-99, 198-202, 267-271

**N-myristoylation site.**

amino acids 43-49, 72-78, 122-128, 210-216

## **FIGURE 59**

CCACCGCGTCCGGGACCGTGGCTGACTAGTTCTAGATCGCGAGCGGCCGCCGGCTC  
AGGGAGGAGCACCGACTCGGCCGCACCTGAGAGATGGTGGTGCCATGTGGAAGGTGATTG  
TTTCGCTGGCTCTGTTGATGCCCTGGCCCTGTGATGGGCTGTTCGCTCCCTATAAGAAGT  
GTTTCCATGCCACCTAACGGAGACTCAGGACAGCCATTATTCTCACCCCTACATTGAAGC  
TGGGAAGATCCAAAAGGAAGAGAATTGAGTTGGTCGGCCCTTCCCAGGACTGAACATGA  
AGAGTTATGCCGGCTTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTGGTT  
TTCCCAGCTCAGATAACAGCCAGAAGATGCCAGTAGTTCTCTGGCTACAGGGTGGCCGG  
AGGTTCATCCATGTTGGACTCTTGTGGAACATGGGCCTATGTTGTCACAAGTAACATGA  
CCTTGCCTGACAGAGACTCCCTGGACCACAACGCTCTCCATGCTTACATTGACAATCCA  
GTGGGCACAGGCTTCAGTTTACTGATGATAACCCACGGATATGCAGTCATGAGGACGATGT  
AGCACGGGATTATACAGTGCACTAATTCAAGTTTCCAGATATTCTGAATATAAAAATA  
ATGACTTTATGTCACTGGGGAGTCTTATGCAGGGAAATATGTGCCAGGCATTGCACACCTC  
ATCCATTCCCTCAACCTGTGAGAGAGGGTGAAGATCAACCTGAACCGAATTGCTATTGGAGA  
TGGATATTCTGATCCGAATCAATTATAGGGGCTATGCAGAATTCTGTACCAAATTGGCT  
TGTTGGATGAGAAGCAAAAAAGTACTTCCAGAACAGCAGTGCATGAATGCATAGAACACATC  
AGGAAGCAGAACTGGTTGAGGCCTTGAAATACTGGATAAAACTACTAGATGGCGACTAAC  
AAGTGATCCTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTTGCCT  
GCACCGAACCTGAGGATCAGCTTACTATGAAATTGTCACTCCAGAGGTGAGACAA  
GCCATCCACGTGGGAATCAGACTTTAATGATGAACTATAGTGAAGAAGTACTTGCAGA  
AGATACAGTACAGTCAAGCCATGGTTAAGTGAATAATTATAAGGTTCTGA  
TCTACAATGGCCAATGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTGATGGC  
ATGGACTGGAAAGGATCCCAGGAATACAAGAACGGAGAAAAAGTTGGAAGATCTTAA  
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGACTCCATCAGGTAATTATTC  
GAGGTGGAGGACATATTACCTATGACCAGCCTCTGAGAGCTTGACATGATTAATCGA  
TTCATTATGAAAAGGATGGATCCTTATGTTGATAAAACTACCTTCCAAAAGAGAACAT  
CAGAGGTTTCATTGCTGAAAAGAAAATGTAAGAACAGAAAATGTCATAGGAATAAAAAAA  
TTATCTTTCATATCTGCAAGATTTCATCAATAAAATTATCCTTGAAACAAGTGAGC  
TTTGTTTGGGGGAGATGTTACTACAAAATTACATGAGTACATGAGTAAGAATTACA  
TTATTAACCTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAAGATGTATAAATGA  
AATTAGGGCTTGAATAGGAAGTTTAATTCTCTAAAGAGTAAGTGAAAAGTGCAGTTG  
TAACAAACAAAGCTGTAACATCTTCTGCCAATAACAGAAGTTGGCATGCCGTGAAGGT  
GTTGGAAATATTATGGATAAGAATAGCTCAATTATCCAAATAATGGATGAAGCTATAA  
TAGTTTGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAACATTCTTGAAATA  
AAAATATTATATAAAAAGTAAAAAAAAAA

## **FIGURE 60**

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPKGDSQPLFLTPYIEAGKIQKGREL  
SVPFPGLNMKSYAGFLTVNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH  
GPYVVTSNMTLDRDFPWTTLMSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQF  
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSILNPVREVKINLNGIAIGDGYSDPESIIGG  
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEEAFEILDKLLDGDLTSDPSYFQNVTG  
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHGNQTFNDGTIVEKYLREDTVQSVKPWLT  
EIMNNYKVLIYNGQLDIIVAAALTERSLMGMDWKGSQEYKKAEKVWKIFKSDSEVAGYIRQ  
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

**Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 81-85, 132-136, 307-311, 346-350

**Casein kinase II phosphorylation site.**

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,  
353-357, 424-428

**Tyrosine kinase phosphorylation site.**

amino acids 423-432

**N-myristoylation site.**

amino acids 22-28, 110-116, 156-162, 232-238

**Serine carboxypeptidases, serine active site.**

amino acids 200-208

**Crystallins beta and gamma 'Greek key' motif signature.**

amino acids 375-391

## FIGURE 61

CGAGGGCTTCGGCTCCGAATGGCACATGTGGAATCCCAGTCTTGGCTACAACAT  
TTTCCCTTCCTAACAGTCTAACAGCTGTTAACAGCTAGTGATCAGGGTTCTTCTT  
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTTG  
CCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGAGTGAGGTGATGGAAG  
TCTAAAATAGGAAGGAATTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC  
CTGGGGAGGGCTGCTAACAGCTTCAAAAAACAGGAGCGACTTCAACTGGCTGGGAT  
AAGACGTGCCGGTAGGATAGGAAGGACTGGTTAGTCCTAACATTGACTGGCTGGG  
TGAACCTAACAGCCTTAACCTCTGGGAGATGAAAACGATGGCTTAAGGGCCAGAAA  
TAGAGATGTTGAAAATAAAATTAAAAAGCAAGTATTTATAGCATAAAGGCTAGA  
GACCAAAATAGATAACAGGATCCCTGAACATTCTAACAGAGGGAGAAAGTATGTTAAAATA  
GAAAAACCAAAATGCGAGAAGGAGGAGACTCACAGAGCTAAACCAGGATGGGACCTGGGTC  
AGGCCAGCCTTTGCTCCTCCGGAAATTATTTGGTCTGACCACTCTGCCTTGTGTTT  
GCAGAATCATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT  
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGCTGGAGGTGG  
ACAGCCGCTGTGGCTCTCAGTGGCTGGGTCTGGCTGGCCCCCAGCAGCCGG  
ATGCCTCAGTCAGCACCTCACTCTGAGAATCGTACTGGACCTTCACCACCTGACCGT  
CCACCAAGGGACGGGGCGTCTATGTGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA  
ACCTGACCATCCAGGTGGCTCATAACAGACAGGGCAGAAGAGGACAACAAGTCTCGTTACCCG  
CCCCTCATCGTGCAGCCCTGCAGCGAAGTGTCTACCCCTACCAACAATGTCAACAAGCTGCT  
CATCATTGACTACTCTGAGAACCGCCTGCTGGCTGTGGAGCCTCTACCAGGGGTCTGCA  
AGCTGCTGCCGGCTGGATGACCTCTCATCCTGGTGGAGCCATCCCACAAGAAGGAGCACTAC  
CTGTCCAGTGTCAACAAGACGGGACCATGTACGGGGTGATTGTGCGCTCTGAGGGTGAGGA  
TGGCAAGCTCTTATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCGACCTGTCCA  
GCCGGAAGCTGCCCGAGACCCCTGAGTCCTCAGCCATGCTGACTATGAGCTACACAGCGAT  
TTTGTCTCCTCTCATCAAGATCCCTCAGACACCCCTGGCCCTGGTCTCCACTTTGACAT  
CTTCTACATCTACGGCTTGCTAGTGGGGCTTGTCTACTTCTCACTGTCCAGCCGAGA  
CCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTACACCTCACGCATCGTGC  
CTCTGCAAGGATGACCCCAAGTCCACTCATACGTGTCCCTGCCCTGGCTGCACCCGGC  
CGGGTGGAAACCGCCTCTGCAGGCTGCTACCTGGCCAAGCCTGGGACTCACTGGCC  
AGGCCTTCAATATCACCAGCCAGGACATGTACTCTTGCATCTCTCAAAGGGCAGAAG  
CACTACCCAGGCGATGACTCTGCCCTGTGCGCTTCCCTACGGGCAACCTGGAGCTCAACTGGC  
GCAGATCAAGGAGCGCCTGCAGTCTGCTACCAGGGCGAGGGCAACCTGGAGCTCAACTGGC  
TGCTGGGAAGGACGTCCAGTGCACGAAGGCGCTGTCCCCATCGATGATAACTCTGTGGA  
CTGGACATCAACCAGCCCTGGAGGCTCAACTCCAGTGGAGGGCTGACCTGTACACCAC  
CAGCAGGGACCGCATGACCTCTGTGCCCTACGTTACAACGGCTACAGCGTGGTTTG  
TGGGACTAAGAGTGGCAAGCTGAAAAGGTAAGAGTCTATGAGTCACTGCTCAAATGCC  
ATTCACCTCCTCAGCAAAGAGTCCCTTGGAGGTAGCTATTGGTGGAGATTTAACTATAG  
GCAACTTATTTCTGGGAACAAAGGTGAATGGGAGGTAAGAAGGGTTAATTGTG  
ACTTAGCTCTAGCTACTCCTCCAGCCATCAGTCATTGGTATGTAAGGAATGCAAGCGTA  
TTCAATATTCCCAAACTTAAGAAAAACTTAAGAAGGTACATCTGCAAAAGCAAA

## **FIGURE 62**

MGTLGQASLFAPPGNYFWSDHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP  
RALEVDSRSVVLLSVVVVLLAPPAAGMPQFSTFHSENRDWTFNHLTQHGTVGAVYVGAINRV  
YKLTGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTLTNNVNKLIIIDYSENRLLAGSL  
YQGVCKLLRLDDLFLILVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGKQDY  
FPTLSSRKLP RDPESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFASGGFVYFL  
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP  
GDSLAQAFNITSQDDVLFIAIFSKGQKQYHHPPDDSAFCPIRAINLQIKERLQSCYQGEQN  
LELNWLLGKDQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG  
YSVVFVGTKSGKLKKVRVYEFRCSNAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

**Signal sequence:**

amino acids 1-32

**Transmembrane domain:**

amino acids 71-87

**N-glycosylation site.**

amino acids 130-134, 145-149, 217-221, 381-385

**Casein kinase II phosphorylation site.**

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,  
384-388, 471-475, 481-485, 530-534

**N-myristoylation site.**

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

## **FIGURE 63**

AGGCTCCCGCGCGCGGCTGAGTGGACTGGAGTGGACCCGGTCCCCCGCGTTAGAGAACACGCG**A**TGACCA  
CGTGGAGCCTCOGGCGGAGGCCGGCCCGCACGCTGGACTCTGCTGCTGGCTCTGGCTTCCTGGCTCC  
GCAGGCTGGACTGGAGCACCCCTGGTCCCTCTGCGGCTCCGCATCGACAGCTGGGCTGCAGGCCAAGGGCTGGA  
ACTTCATGCTGGAGGATTCCACCTCTGGATCTCGGGGCTCCATCACTATTTCGTGTGCCAGGGAGTACT  
GGAGGGACCGCCCTGCTGAAGATGAAGGCCCTGCTGAACACCCTCACACCTATGTTCCGTGGAACCTGCATG  
AGCCAGAAAGAGGCAAATTGACTTCTCTGGGAACCTGGACCTGGAGGCCCTCGTCTGATGGCCGCAGAGATCG  
GGCTGTGGGTATTCTGCTCCAGGCCCTACATCTGCTGAGATGGACCTCGGGGCTGCCAGCTGGCTAC  
TCCAAGACCCCTGGCATGAGGCTGAGGACAACCTAACAGGGCTCACCGAAGCAGTGGACCTTATTGACCACC  
TGATGTCCAGGGTGGTGCCACTCCAGTACAAGCGTGGGGAGCTATCGTGGCTGAGGTGAGAAATGAATATG  
GTTCTATAATAAAGACCCCGCATACATGCCCTACGTCAAGAAGGCCTGGAGGACCGTGGCATTGTGGAACCTGC  
TCCTGACTTCAGACAACAAGGATGGGTGAGCAAGGGATTGTCCAGGGAGTCTTGGCCACCATCAACTTGCAGT  
CAACACACGAGCTGCAGCTACTGACCACCTTCTCTTCAACGTCCAGGGAGCTCAGCCCAAGATGGTGTGGAGT  
ACTGGACGGGGTGGTTGACTCGTGGGAGGCCCTCACAAATATCTTGGATTCTCTGAGGTTTGAAAACCGTGT  
CTGCCATTGTGGACGCCGCTCCATCAACCTCTACATGTTCCACGGAGGCACCAACTTGGCTTCATGAATG  
GAGCCATGCACTCCATGACTACAAGTCAGATGTCACCAGCTATGACTATGATGCTGTGCTGACAGAACCGCG  
ATTACACGCCAAGTACATGAAGCTTCGAGACTCTCGGCTCCATCTCAGGCATCCCTCTCCCTCCCCACCTG  
ACCTTCTTCCAAGATGCCGTATGAGCCCTTAACGCCAGTCCTGTACCTGTCTGTGGACGCCCTCAAGTACC  
TGGGGAGCCAATCAAGTCTGAAAAGCCATCAACATGGAGAACCTGCCAGTCATGGGGAAATGGACAGTCCT  
TCGGGTACATTCTCTATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCCACGTGCTGATCGGGGGCAGG  
TGTTTGTGAACACAGTATCCATAGGATTCTGGACTACAAGACAACGAAGATTGCTGTCCCCCTGATCCAGGGTT  
ACACCGTGTGAGGATCTGGTGGAGAATCGTGGCGAGTCACATGGGGAGAAATTGATGACCAGCGCAAAG  
GCTTAATTGGAAATCTCTATCTGAATGATTACCCCCTGAAAAACTTCAGAATCTATAGCCTGGATATGAAGAAGA  
GCTTCTTCAGAGGTTGGCCTGGACAAATGGNTTCCCTCCAGAAACACCCACATTACCTGCTTCTTCTTGG  
GTAGCTTGTCCATCAGCTCACGCCCTGTGACACCTTCTGAAGCTGGAGGGCTGGAGAAGGGGTTGTATTCA  
TCAATGCCAGAACCTTGGACGTTACTGGAACATTGGACCCAGAACAGCCTTACCTCCAGGTCCCTGGTTGA  
GCAGCGGAATCAACCAGGTATCGTTTGAGGGAGACGATGGGGCCCTGCATTACAGTTACGGAAACCCCCC  
ACCTGGGAGGAACCACTACATTAAGT**G**AGCGGTTGGCACCCCTCTGCTGGTGCAGTGGGAGACTGCCGCTC  
CTCTTGACCTGAAGCCTGGCTGCTGCCCAACCCCTCAGTCAGCAGAACCTTAAGCTGGCAGGGATGGCTCTGGGCC  
ACTGGGGCTACAGTCTGCCCTGTCTCAGTCAGCTAACACCCCTAAGCCTGAGGGAAAGGTGGATGGCTCTAGGGTGGAGC  
TGGCTTGTGATGGCTTCTCACAGCCCTGCTCTGTGCGGAGGCTGTGGCTGTCTAGGGTGGAGC  
AGCTAATCAGATGCCAGCCTTGGCCCTCAGAAAAAGTGTGAAACAGTGCCTTCAGCCGACGTACAGCCC  
TGCAGCATCTGCTGGACTCAGCGTGCTCTTGCTGGTCTGGAGGCTGGCCACATCCCTCATGGCCCCAT  
TTTATCCCCGAATCCTGGGTGTGTCACAGTGTAGAGGGTGGGAAGGGGTGTCTCACCTGAGCTGACTTGT  
CTTCCCTCACAAACCTCTGAGCCTCTTGGGATTCTGAAGGAACCTGGCGTGAAGAACATGTGACTTCCCC  
TCCCTCCCACTCGCTGCTCCCACAGGGTACAGGCTGGAGAAACAGAACCTCACCCCTGCGTCTTCC  
CAAGTTAGCAGGTGTCTGGTCACTGAGGAGGACATGTGAGTCTGGCAGAACGCCATGCCCATGTCTGCA  
CATCCAGGGAGGAGGACAGAACGGCCAGCTCACATGTGAGTCTGGCAGAACGCCATGCCCATGTCTGCAACATCC  
AGGGAGGAGGACAGAACGGCCAGCTCACATGTGAGTCTGGCAGAACGCCATGCCCATGTCTGCAACATCCAGGG  
GGAGGACAGAACGGCCAGCTCACATGTGAGTCTGGCAGAACGCCATGCCCATGTCTGCAACATCCAGGGAGG  
ACAGAACGGCCAGCTCAGTGGCCCCGCTCCCCACCCCCCACGCCGAACAGCAGGGCAGAGCAGCCCTCTTC  
GAAGTGTGTCAGTCCGATTTGAGCCTTGTCTGGGCCAGCCAAACACCTGGCTTGGCTACTGCTG  
GTTGCAGTAAAGCTATAACCTTGAATCACAA

## **FIGURE 64**

MTTWSLRRR PARTLGLLLLVVLGFLVLRRLDWSTLVPLRLRHQLGLQAKGWNFMLEDSTFW  
IFGGSIHYFRVPREYWRDRLLKMKACGLNTLTTYVPWNLHEPERGKFDFSGNLDLEAFVLMA  
AEIGLWVILRPGPYICSEMDLGGLPSWLLQDPGMRLRTTYKGFTEAVIDLYFDHLMMSRVVPLQ  
YKRGGPIIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLTSNDKDGLSKGIVQGVLAT  
INLQSTHELQLLTTFLNVQGTQPKMVMEYWTGFDSWGGPHNILDSSEVLKTVSAIVDAGS  
SINLYMFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDYTAKYMKLRDFFGSISGIP  
LPPPPDLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGGNGQSFYIYE  
TSITSSGILSGHVHDRGQVFVNTVSIGFLDYKTTKIAVPLIQGYTVLRILVENRGRVNYGEN  
IDDQRKGLIGNLYLNDSPLKNFRIYSLDMKKSFFQRFGLDKWXSLPETPTLPAFFLGSLYSIS  
STPCDTFLKLEGWEKVVFinQNLGRYWNIGPQKTLYLPGPWLSSGINQVIVFEETMAGPA  
LQFTETPHLGRNQYIK

**Signal sequence:**

amino acids 1-27

**Casein kinase II phosphorylation site.**

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

**N-myristoylation site.**

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,  
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

## FIGURE 65

GGGGACGGGAGCTGAGAGGCTCCGGCTAGCTAGGTGTAGGGTGGACGGTCCCAGGACC  
CTGGTGAGGGTTCTCTACTTGGCCTCGGTGGGGTCAAGACGCAGGCACCTACGCCAAAGG  
GGAGCAAAGCCGGCTCGGCCGAGGCCCGAGGACCTCATCTCCAATGTTGGAGGAATC  
CGACACGTGACGGTCTGTCGCCGTCTCAGACTAGAGGAGCGCTGAAACGCCATGGCTCC  
AAGAAGCTGTCCTGCCTCGTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCA  
GGCAGACACTCGGTCGTTGCTAGGGATAGGGGTCATGACCGGTTCTCCTAGACGGGCC  
CGTCCGCTATGTGTCGGCAGCCTGCACTACTTCGGGTACCGCGGGTGCTTGGGCCAC  
CGGCTTTGAAGATGCGATGGAGCGGCCTCAACGCCATACAGTTATGTCGCCCTGGAACTA  
CCACGAGCCACAGCCTGGGGTCTATAACTTAATGGCAGCCGGACCTCATGCCCTTCTGA  
ATGAGGCAGCTCTAGCGAACCTGTTGGTCATACTGAGACCAAGGACCTACATCTGTGCAGAG  
TGGGAGATGGGGGGTCTCCCATCCTGGTTGCTCGAAAACCTGAAATTCTAAGAACCTC  
AGATCCAGACTCCTGCGCAGTGACTCCTGGTTCAAGGTCTGCTGCCAAGATATATC  
CATGGCTTATCACAAATGGGGCAACATCATTAGCATTAGGTGGAGAATGAATATGGTAGC  
TACAGAGCCTGTGACTTCAGCTACATGAGGCACCTGGCTGGCTCTCGTGCACTGCTAGG  
AGAAAAGATCTGCTCTCACACAGATGGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG  
GAECTATACCACTGTAGATTGGCCAGCTGACAACATGACCAAAATCTTACCCCTGCTT  
CGGAAGTATGAACCCATGGGCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTA  
CTGGGGCCAGAATCACTCCACACGGTCTGTGTCAGCTGTAACCAAGGACTAGAGAACATGC  
TCAAGTTGGGAGCCAGTGTGACATGTACATGTTCCATGGAGGTACCAACTTGGATATTGG  
AATGGTGCCGATAAGAAGGGACGCTCCCTCGATTACTACCAGCTATGACTATGATGCACC  
TATATCTGAAGCAGGGGACCCACACCTAACGCTTTGCTCTCGAGATGTACAGCAAGT  
TCCAGGAAGTCCCTTGGGACCTTACCTCCCCGAGCCCCAAGATGATGCTGGACCTGTG  
ACTCTGCACCTGGTTGGCATTACTGGCTTCTAGACTTGCTTGGCCCCGTGGGCCAT  
TCATTCAATCTGCCAATGACCTTGAGGCTGTCAGCAGGACCATGGCTCATGTTGTACC  
GAACCTATATGACCCATACCATTGGAGCCAACACCATTCTGGGTGCCAATAATGGAGTC  
CATGACCGTGCCTATGTGATGGTGGATGGGTGTTCCAGGGTGTGGAGCGAAATATGAG  
AGACAAACTATTTTGACGGGAAACTGGGTCAAACCTGGATATCTGGTGGAGAACATGG  
GGAGGCTCAGCTTGGGTCTAACAGCAGTGACTCAAGGGCCTGTTGAAGCCACCAATTCTG  
GGGCAAACAATCCTAACCACTGGATGATGTTCCCTCTGAAAATTGATAACCTGTGAAGTG  
GTGGTTCCCTCCAGTTGCCAAATGCCATATCCTCAAGCTCCTCTGGCCCCACATTCT  
ACTCCAAAACATTCCAATTAGGCTCAGTTGGGGACACATTCTATATCTACCTGGATGG  
ACCAAGGGCAAGTCTGGATCAATGGGTTAACCTGGGCCGGTACTGGACAAAGCAGGGCC  
ACAACAGACCCCTACGTGCCAAGATTCTGCTGTTCTAGGGAGCCCTAACAAAATTA  
CATTGCTGGAACCTAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTGGATAAGCCTATC  
CTCAATAGCACTAGTACTTGACAGGACACATCAATTCCCTTCAGCTGATAACTGAG  
TGCCTCTGAACCAATGGAGTTAAGTGGCACTGAAAGGTAGGCCGGCATGGTGGCTCATGC  
CTGTAATCCCAGCACTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAAGGACTTCAAGA  
CCAGCCTGGCCAACATGGAAACCCCGTCTCCACTAAAAAATACAAAATTAGCCGGCGTG  
ATGGTGGGCACCTCTAATCCCAGCTACTGGGAGGCTGAGGGCAGGAGAATTGCTTGAATCC  
AGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTACCACTGCACTCCAGCCTGGCTGACAGTGA  
GACACTCCATCTCAAAAAAAAAAA

## **FIGURE 66**

MAPKKLSCLRSLLLPLSLTLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL  
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVNFNGSRDLIAFLNEAALANLLVILRPGPYI  
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE  
YGSYRACDFSYMRHLAGLFALLGEKILLFTTDGPEGLKCGSLRGGLYTTVDFGPADNMTKIF  
TLLRKYEPhGPLVNSEYYTGWLWQNHSTRSAVTKGLENMLKLGASVNMYMFHGKTNF  
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPGLPLPPSPKMML  
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTPFWVPN  
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLSFGSNSSDFKGLLKP  
PILGQTILTQWMMFPLKIDNLVWWFPLQLPKWPYQAPSGPTFYSKTFPILGSVGDTFLYL  
PGWTKGQVWINGFNLGRYWTQGPQQTLYVPRFLFPRGALNKITLLELEDVPLQPQVQFLD  
KPILNSTSTLHRTHINSLSADTLSASEPMELSGH

**Signal sequence:**

amino acids 1-27

**N-glycosylation site.**

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 4-8

**Casein kinase II phosphorylation site.**

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,  
603-607, 644-648

**Tyrosine kinase phosphorylation site.**

amino acids 191-198

**N-myristoylation site.**

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,  
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

## **FIGURE 67**

GCTTGAAACACGTCTGCAAGCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTCAGTGC  
ACCCACAATATGGCTTACATGTTAAAAAGCTTCTCATCAGTTACATATCCATTATTGTGT  
TTATGGCTTATCTGCCTCTACACTCTCTGTTATTCAAGGATAACCTTGAAGGAATATT  
CTTCGAAAAGTCAGAGAAGAGAGCAGTTAGTGCACATTCCAGATGTCAAAACGATT  
GCGTCCTTCTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTGGTGTGTT  
CTTGTCAAGAGTTAGTGAAGAAATAACTAGGGAAATTAGTTGAACCATGAGTGGACATTG  
AAAAACTCAGGCAGCACATTCAACGCCAGGACAAGCAGGAGTTGCATCTGTTCATG  
CTGTCGGGGTGCCCCATGCTGTCTTGACCTCACAGACCTGGATGTGCTAAAGCTTGA  
AATTCCAGAAGCTAAAATTCTGCTAACAGATTCTCAAATGACTAACCTCAAGAGCTCCACC  
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTAGCTTCTCGCGATCACTGAGA  
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCTGCCTGGGTGTATTGCTAAAAAA  
CCTTCGAGAGAGTTGTACTTAATAGGCAATTGAACCTCTGAAAACAATAAGATGATAGGACTTG  
AATCTCTCCGAGAGTTGGCACCTTAAGATTCTCACGTGAAGAGCAATTGACCAAAGTT  
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTATAATGACGGCAC  
TAAACTCTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACTCCAGA  
ACTGTGAGCTAGAGAGAATCCCACATGCTATTTCAGCCTCTCTAACAGGAACTGGAT  
TTAAAGTCCAATAACATTGCACAATTGAGGAAATCATCAGTTCCAGCATTAAAACGACT  
GACTTGTAAAATTATGGATAACAAAATTGTTACTATTCCCTCCCTATTACCCATGTCA  
AAAACTTGGAGTCACTTATTCTCTAACACAAGCTCGAACCTTACAGTGGCAGTATT  
AGTTACAGAAACTCAGATGCTTAGATGTGAGCTACAACAACATTCAATGATTCAATAGA  
AATAGGATTGCTTCAGAACCTGCAGCATTTGCATATCACTGGAACAAAGTGGACATTCTGC  
CAAACAAATTGTTAAATGCATAAAGTTGAGGACTTGAATCTGGACAGAACTGCATCACC  
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGAACTG  
CTTGGACCGCCTGCCAGCCCAGCTGGCCAGTGTGGATGCTCAAGAAAAGCGGGCTGTTG  
TGGAAGATCACCTTTGCAAATGGATTAAAACTAACAGATAATATGACACAGTGTGCAGGAAC  
AACTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTAGGAGTAG  
ATACATCTTTAAAATAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT  
GTTCAATGTTGTTAGGGTTAAAGTCATTCACTTCCAAATCATTGTTCTTTGGG  
AAAGGGAAGGAAAATTATAACTAAATCTTGGTTCTTTAAATTGTTGTAACCTGGAT  
GCTGCCGCTACTGAATGTTACAAATTGCTTGCCTGCTAAAGTAAATGATTAAATTGACATT  
TTCTTACTAAAAAAAAAAAAAA

## **FIGURE 68**

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPLKEYSFEKVREESSFSDIPDVKNDFAFL  
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLRQHISRNAQDKQELHLFMLSG  
VPDAVFDTLDVLKLELIPEAKIPAKISQMNTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH  
VKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMIGLESLRELRLKILHVKSNLTKVPSN  
ITDVAPHLTKLVIHNDGTKLLVLNSLKKMMNVAELELQNCELERIPHAIFSLSNLQELDLKS  
NNIRTIEIIISFQHLKRLTCLKLWHNKIVTISSITHVKNLESLYFSNNKLESLPVAVFSLQ  
KLRCLDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP  
EKVGQLSQLTQLELKGNCLDRPAQLGQCRMLKKSGLVVEDHLFDTLPLEVKEALNQDINIP  
FANGI

**Signal sequence:**

amino acids 1-20

**N-glycosylation site.**

amino acids 241-245, 248-252, 383-387

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 326-330

**Casein kinase II phosphorylation site.**

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

**Tyrosine kinase phosphorylation site.**

amino acids 349-355, 375-381

**N-myristoylation site.**

amino acids 78-84, 124-130, 212-218, 392-398

## **FIGURE 69**

CC CAC CG CG TCC GGC CT TCT CT GG ACT TT GC AT TT CC AT TT CATT GA CA AA ACT GA CT TT TT ATT CT  
TTT TT CC AT CT CT GG CC AG CT GG AT CC TAGG CG CC CT GG AAG AC AT TT GT GT TT AC AC AC TA AGG AT  
CT GT GT TT GG GG TT CT T CT CC CT GG AC AT TT GG CATT GC TTA GT GG CT TG GT GG GG AG GG ACC AC CG TG  
G CTC AGT G CTT GC TT GC ACT TAT CT GC CT AGG TA CAT CGA AGT CT TT GA CCT CC AT AC AGT G ATT AT GC CT GT  
AT CG CT GG GT AT CT GG CC CT TT GC CT GT GC AT AGT GT GT CG CT TG CT GT CT TT ACT TCA AA AT AC AC AAC  
GCG CTA AA AG CT GCAA AGG AAC CT GA AG CT GT GG CT GT AAA AA AT CACA ACC CAG AC AAG GT GT GG GT GG CC AG  
AAC AG CC AGG CCAA ACC AT GC CAC CG AGT CT GT GC CT GG CG ACT GT GT GA AGG AT AT AGA AT GT GT GC  
AG TT TT GA TT CC CT GC CAC CT GT GT GC GA CAT AA AT GA GGG CT CT GA GT TAGG AAGG CT CC CT TC CAA  
GC AG AG CC CT GA AG AC TT CA AT GT CA AT GA GG CC AC CT GT TT GT AT GT GC AGG CAC AG AAG GAA AGG CAC AG  
CT CC CC AT CAG TT CAT GG AAA AT AACT CAGT GC CT GT GG AACC AG CT GT GG AG AT CC CT AC AG AG AG CT TC  
CA CT GG GG CA ACC CT CC AGG AAGG AGT GT GG AG AG AACC CT ACT GT GG GG AT GT GT AT AA ACC AGT CA  
CAC AG CT GC CT TATT CT CA CAA AT CT ACC CC TT GC GT GG ACT GAC GT TT CC CT GG AG GT GT CC AG AAA  
GCT GA GT TA AC AC AG AG CC TATA AA AG CT GT CG CT TA AGG CT GC CC AG GC CC TT GC CAA AT GG AG CT GT  
AGA AGG CT CAT GC CATT GA CC CT TT AA TT CT CT GT TT GG CG AG CT GCA AT GG CG AGG CT GA AGG CA AT  
GCA AG CT GC AC AGT CAGT CT AGG GG GT GC CA AT AT GG CAG AG ACC CAA AG CC AT GAT CC TGT CA ACT CA AT CCC  
AGT GAG AACT GC AC CT GG CA AT AGA AG ACC CAA ACC AG CAT CAG AATT AT CT TT CT AT GT CC AGC TT  
GAT CC AG AT GG AAG CT GT GAA AGT GAAA AC AT TA AGT CT TT GA CGG A AC CT CC AG CA AT GG CC CT TG CT AG GG  
CA AGT CT GC AG TAAA AC GACT AT GT CT CT GT ATT TGA AT CAT CAGT AC ATT GA CG TT CAA AT AGT TACT  
GA CT CAG CA AG AATT CAA AG AACT GT CT TT GT CT TACT ACT TT CT CT CTA AC AT CT CT AT TCC AA ACT GT  
GG CG GT TA CCT GG AT AC CT TT GG AAGG AT CCT CACC AG CCCC AT TA CCA AA AG CC GCA T CT GAG CT GG CT TAT  
TGT GT GT GG CA CATA CA AGT GG AGA AA AG ATT ACA AG AATA ACT AA ACT CAA AG AG AT TT CC TAGA AA AT AG AC  
AA AC AGT G CAA AT TT GAT TT CT GC CAT CT AT GA TGG CC CT CC ACC AACT CT GG CT GAT GG ACA AGT CT GT  
GG CG GT GACT CCC AC CT TC GA AT CGT CAT CAA ACT CT CT GA CT GT CG TT GT CT AC AGA TT AT GC CA AT CT  
TAC CG GG GAT TT CT GT CT TT CT AC AC CT CA ATT TAT GC AG AAA AC AT CA AC ACT AC AT CT TA ACT TG CT TT CT  
GAC AGG AT GAG GT TATT ATA AG CAA AT CCT AC CT TAG AGG CT TT TA ACT CT TA AT GG AATA ACT TG CA ACT AAA  
GAC CCA ACT TG CAG ACC AAA ATT TAT CAA AT GT GT GG AT TT CT GT CC CT TA AT GG AT GT GG TACA AT CAGA  
AAG GT AGA AG AT CAGT CA ATT ACT TA CAC CA AT TA AT CAC CT TT CT GC AT CCT CA ACT CT GA AGT GT GAT CACC  
CGT CAG AA AC AACT CC CAG ATT ATT GT GA AGT GT GAA AT GG GAC AT TA AT CT AC AGT GG AG AATA AT AC AT AACA  
GA AG AT GAT GT AAT ACA AA AGT CAA AA GCA CT GG GCA AA AT TA AC ACC CAG AT GG CT TT TT GA AT CC AATT CA  
TTG AAA AG ACT AT ACT TG AAT CAC CA TATT AT GT GG ATT TG AAC CAA ACT CT TT GT CA AGT TAGT CT GC AC  
AC CT CAG AT CCA AT TT GG GT GT TT CT TGA TAC CT GT AG AG CTC TCC CAC CT GT ACT TT GC AT CCT CA ACC  
TAC GAC CCT AAT CA AAG AGT GG AT GT TAGT CG AG AT GAA ACT TT GT AAG GT TAT CC TT ATT TG GAC ACT AT GG GAGA  
TT CC AG TT TA AT GC CT TT AA ATT CT TG AGA AGT AT GAG CT CT GT TAT CT GC AGT GT AA AG TT GT GAT AT GT GAT  
AGC AGT GACC ACC AGT CT CG CT GC AAT CA AGG TT GT CT CC AGA AG CAA AC GAG AC AT TT CT TCA TATA AA AT GG  
AAA AC AG AT TCC AT CAT AGG ACC CATT CG CT GAAA AGGG AT CGA AGT GCA AGT GG CA AT TC AGG AT TT CAG CAT  
GAA AC AC AT CG GG AAG AA ACT CCA AA ACC AGC CCT TCA AC AGT GT GC AT CT GT TT CT CT AT GG TT CT AG CT TG  
AAT GT GG GT ACT GT TAGC GACA AT CA CAGT GAGG AT TT GT AA AT CA AC GGG CAG ACT ACA AA AT ACC AGA AG CT G  
CAG AACT AT AA ACT AAC AGG TCCA ACC CT AAGT GAG AC AT GT TT CT CC AGG AT GC CAA AGG AA AT GT CT AC CT CG  
GG CT AC AC AT ATT AT GA AT AA AT GA GGG CCGT GAA AGT GAC AC AC AGG CCGT GC AT GT AAAA AAAAA

## **FIGURE 70**

MELVRRLMPLTLLLILSCLAEALTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI  
ERPENKSIRIIFSYVQLDPDGSCESENIKVFDGTSSNGPLLGQVCSKNDYVPVFESSSTLT  
FQIVTDSARIQRTVFVFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQV  
EKDYKIKLNFKEIFLEIDKQCKFDLAIYDGPSTNSGLIGQVCGRTPTFESSNSLTVVLS  
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMVIISKSYLEAFNSNGNNLQLKDPTCRP  
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIIITFSASSTSEVITRQKQLQIIVKCEMGHNST  
VEIIYITEDDVIQSQNALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFVQVSLHTSDPN  
LVVFLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNFKFLRSMSSVYL  
QCKVLICDSSDHQSRCNQGCVSRSKRDIISSYKWKTDSIIGPIRLKRDRSASGNQFHETHA  
EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

**Signal sequence:**

amino acids 1-24

**Transmembrane domain:**

amino acids 571-586

**N-glycosylation site.**

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,  
394-398, 419-423

**Casein kinase II phosphorylation site.**

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,  
408-412, 463-467, 520-524, 556-560

**Tyrosine kinase phosphorylation site.**

amino acids 172-180, 407-415, 407-416, 519-528

**N-myristoylation site.**

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## **FIGURE 71**

GACGGAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCTGCGCCG  
GGACATGCGGCCCCAGGAGCTCCCCAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGC  
TGCTGCGCCGCCGTGCCCTGCCAACAGCGCCACGCGCTTCGACCCCCACCTGGGAGTCC  
CTGGACGCCGCCAGCTGCCCGTGGTTGACCAAGGCAAGTCGGCATCTTCATCCACTG  
GGGAGTGTTCGCCCAGCTCGGTAGCGAGTGGTTCTGGTGGTATTGGAAAAGGAAA  
AGATACCGAAGTATGTGAAATTATGAAAGATAATTACCCCTAGTTCAAATATGAAGAT  
TTTGGACCACATTACAGCAAATTTTAATGCCAACAGTGGCAGATATTTCAAGGC  
CTCTGGTGCCTAACATTCAGCTTAACCTCCAAACATCATGAAGGCTTACCTGTGGGGT  
CAGAATATTCTGTGGAACCTGGAAATGCCATAGATGAGGGGCCAAGAGGGACATTGTCAAGGAA  
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCGTTGGACTGTACTATTCCCTTTGA  
ATGGTTTATCCGCTTCTGAGGATGAATCAGTCATTCCATAAGCGGCAATTCCAG  
TTCTAAGACATTGCCAGAGCTATGAGTTAGTGAACAACATCAGCCTGAGGTTCTGTGG  
TCGGATGGTGACGGAGGAGCACCGGATCAAACTGGAACAGCACAGGCTTCTGGCCTGGTT  
ATATAATGAAAGCCCAGTCGGGGCACAGTAGTCACCAATGATCGTTGGGAGCTGGTAGCA  
TCTGTAAGCATGGTGGCTTCTACCTGCAGTGATCGTTATAACCCAGGACATCTTGCCTA  
CATAAATGGAAAAGTGCATGACAATAGACAAACTGCTGGGCTATAGGAGGGAAAGCTGG  
AATCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTGTAGAGACAGTTCATGTG  
GAGGAAATCTTGATGAATATTGGGCCACACTAGATGGCACCATTTCTGTAGTTTGAG  
GAGCGACTGAGGCAAGTGGGCTGGCTAAAGTCAATGGAGAAGCTATTATGAAACCTA  
TACCTGGCGATCCCAGAATGACACTGTACCCCCAGATGTGTGGTACACATCCAAGCCTAAAG  
AAAAATTAGTCTATGCCATTCTTAAATGGCCCACATCAGGACAGCTGTTCTGGCCAT  
CCCAAAGCTATTCTGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAAC  
GATTCTTGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACATTATCAGATGC  
CGTGTAAATGGGCTGGCTTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG  
ATGCTGCAAGTTATGTCTAAGGCTAGGAACATCAGGTGTCTATAATTGTAGCACATGGAGA  
AAGCAATGTAACGGATAAGAAAATTATTGGCAGTTCAAGCCCTTCCCTTTCCACTA  
AATTCTTAAATTACCCATGTAACCATTAACTCTCCAGTGCACTTGCCATTAAAGTC  
TCTTCACATTGATTGTTCCATGTGTGACTCAGAGGTGAGAATTTCACATTATAGTAG  
CAAGGAATTGGTGGTATTATGGACCGAAGTGAAGAAATTATGTTGAAGCCATATCCCCCATG  
ATTATATAGTTATGCATCACTTAATATGGGATATTCTGGAAATGCATTGCTAGTCAT  
TTTTTTGTGCAACATCATAGAGTGTATTACAAATCTAGATGGCATAGCCTACTACA  
CACCTAATGTGTATGGTATAGACTGTTGCTCCTAGGCTACAGACATATACAGCATGTTACTG  
AATACTGTAGGCAATAGTAACAGTGGTATTGTATATCGAAACATATGGAAACATAGAGAAG  
GTACAGTAAAATACTGTAAAATGGTGCACCTGTATAGGGCACTTACACGAATGGAG  
CTTACAGGACTGGAAGTTGCTGGGTGAGTCAGTGAATGTGAAGGCCTAGGACATTA  
TTGAACACTGCCAGACGTTATAAATACTGTATGCTTAGGCTACACTACATTATAA  
GTTTTCTTCTCAATTATAAACATAAGTGTACTGTAACATTACAAACGTTTAATT  
TTTAAACCTTTGGCTTTGTAATAACACTAGCTAAACATAACTCATTGTGCAA  
ATGTAA

## **FIGURE 72**

MRPQELPRLAFPLLLLLLPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIFIHWG  
VFSVPSFGSEWFWWYWKKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAKFFNANQWADIFQAS  
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRGFLYYSLFEW  
FHPLFLEDESSSFHKRQFPVSRTLPELYELVNYYQPEVLWSDGDGGAPDQYWNSTGFLAWLY  
NESPVVRGTVVTNDRGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI  
SDYLTIEELVKQLVETVSCGGNLLMNIPTLDGTISVVFEERLRQVGWLKVNGEAIYETYT  
WRSQNNDTVTPDVWYTSPKPEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI  
SLEQNGIMVELPQLTIHQMPCKWGWLALTNVI

**Signal sequence:**

amino acids 1-28

**N-glycosylation site.**

amino acids 171-175, 239-243, 377-381

**Casein kinase II phosphorylation site.**

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,  
375-375

**Tyrosine kinase phosphorylation site.**

amino acids 361-369, 389-397

**N-myristoylation site.**

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

**Leucine zipper pattern.**

amino acids 410-432

**Alpha-L-fucosidase putative active site.**

amino acids 283-295

## **FIGURE 73**

AGCAGGGAAATCCGGATGTCTCGTTATGAAGTGGAGCAGTGAGTGTGAGCCTAACATAGT  
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAAGTGGCCATC  
TGAGGTGTTCCCTGGCTCTGAAGGGTAGGCACGATGGGCAGGTGCTTCAGCCTGGTGTG  
CTTCTCACTTCCATCTGGACCACAGGGCTCTGGTCCAAGGCTCTTGCAGCAGAAGAGCT  
TTCCATCCAGGTGTATGCAGAATTATGGGATCACCCCTGTGAGCAAAAGGCGAACAGC  
AGCTGAATTACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGACTAAGTTGGCGGCAAG  
GACCAAGTTGAAACAGCCTGAAAGCTAGCTTGAAACTTGCAGCTATGGCTGGGTTGGAGA  
TGGATTCGTGGTCATCTTAGGATTAGCCAAACCCCAAGTGTGGAAAAATGGGTTGGGTG  
TCCTGATTGAAAGGTTCCAGTGAGCCGACAGTTGCAGCCTATTGTTACAACACTCATCTGAT  
ACTTGGACTAACTCGTGCATTCCAGAAATTATCACCACCAAAGATCCCATAATTCAACACTCA  
AACTGCAACACAAACACAGAAATTATTGTCAAGTGCAGTACACTCGGTGGCATCCCCTT  
ACTCTACAATACCTGCCCTACTACTACTCCTCTGCTCCAGCTCCACTTCTATTCCACGG  
AGAAAAAAATTGATTGTGTACAGAAGTTTATGGAAACTAGCACCAGTCTACAGAAAC  
TGAACCATTGTTGAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTGGAGGTGTCC  
CCACGGCTCTGCTAGTGCTCTCCTCTTGGTGTGCAGCTGGTCTGGATTTGC  
TATGTCAAAAGGTATGTGAAGGCCCTCCCTTTACAAACAAGAATCAGCAGAAGGAAATGAT  
CGAAACCAAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCATAATGAGGAATCAAAGA  
AAACTGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCCGGAA  
GCTGAAGTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTTCATGCTCC  
TTACCCCTGCCCAAGCTGGGAAATCAAAGGGCAAAGAACCAAGAACAGTCCACCCCTT  
GGTTCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAACG  
CCTTCTCCTATTGTAACCCTGCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCC  
TTCTAGCCTGGCTATGTCTTAATAATATCCCACGGAGAACAGGAGTTTGCAAAGTGCAA  
GGACCTAAAACATCTCATCAGTATCCAGTGGTAAAAGGCCCTGGCTGTGAGGCTAGG  
TGGTTGAAAGCCAAGGAGTCAGGACTGAGACCAAGGCTTCTACTGATTCCGAGCTCAGAC  
CCTTCTCAGCTCTGAAAGAGAACACGTATCCCACCTGACATGCTCTGAGGCCGGTA  
AGAGAAAAGAACATGGCAGAAAAGTTAGCCCCTGAAAGCCATGGAGATTCTCATAACCTGAG  
ACCTAATCTCTGTAAGCTAAAATAAAGAAATAGAACAGGCTGAGGATACGACAGTACACT  
GTCAGCAGGGACTGTAAACACAGACAGGGCAAAGTGTCTCTGAACACACATTGAGTTGGA  
ATCACTGTTAGAACACACACACTTACTTTCTGGTCTCTACCACTGCTGATATTCTCT  
AGGAAATATACTTTACAAGTAACAAAATAAAACTCTTATAAATTCTATTCTATCTGA  
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTGTTAAAAGTAATAAAATTCA  
ACAAACATTGCTGAATAGCTACTATGTCAGTGCTGTGCAAGGTATTACACTCTGTAAT  
TGAATATTATTCTCAAAAATGCACTAGTAGAACGCTATCTGGGAAGCTATTCTCT  
GTTTGATATTCTAGCTTATCTACTTCCAAACTAATTCTATTCTGAGACTAATCTT  
ATTCAATTCTCTAATATGGCAACCATTATAACCTTAATTATTAAACATACCTAACAG  
TACATTGTTACCTCTATATACCAAAGCACATTAAAAGGCCATTAAACAAATGTATCACTA  
GCCCTCCTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATTGTGACAAAAATTAA  
AGCATTAGAAAACCTT

## **FIGURE 74**

MARCFSLVLLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR  
LLGLSLAGKDQVETALKASFETCSYGVGDGFVVISRISPNSPKCGKNGVGVLIWKPVSQF  
AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPP  
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAASFNEAAGFGGVPTALLVIALLFF  
GAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKTDKNPEESKSP  
SKTTVRCLAEAV

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site.**

amino acids 53-57, 130-134, 289-293

**Casein kinase II phosphorylation site.**

amino acids 145-149, 214-218

**Tyrosine kinase phosphorylation site.**

amino acids 79-88

**N-myristoylation site.**

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

## **FIGURE 75**

AGATGGCGGTCTTGGCACCTCTAATTGCTCTCGTATTGGTGCACGACTTCACGATGG  
CTCGCCCAACCTTACTACCTCTGTCGGCCCTGCTCTGCTGCCCTACTCGTGAGGAA  
ACTGCCGCCGCTCTGCCACGGTCTGCCACCCAACCGGAAGACGGTAACCGTGTGACTTTG  
ACTGGAGAGAAGTGGAGATCCTGATGTTCTCAGTGCCATTGTGATGAGAAGAACCGCAGA  
TCCATCACTGTGGAGCAACATATAGGCAACATTTCATGTTAGTAAAGTGGCAACACAAT  
TCTTTCTTCCGCTTGGATATTGCATGGCCTACTTACATCACACTCTGCATAGTGTCC  
TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA  
ACCATTGATGAGGAACTAGAACGGGACAAGAGGGTCACTGGATTGTGGAGTTCTTGCAA  
TTGGTCTAATGACTGCCAATCATTGCCCTATCTATGCTGACCTCTCCCTAAATACAAC  
GTACAGGGCTAAATTTGGGAGGTGGATGTTGGACGCTACTGATGTTAGTACGGGTAC  
AAAGTGAGCACATCACCCCTACCAAGCAACTCCCTACCCCTGATCCTGTTCCAAGGTGGCAA  
GGAGGCAATGCGGCGGCCACAGATTGACAAGAAAGGACGGCTGTCTCATGGACCTCTG  
AGGAGAATGTGATCCGAGAATTAACTAAATGAGCTATACCAGCGGCCAAGAAACTATCA  
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTCAACCCCCACCACAGTGTCA  
TGGGAAAACAAGAAGGATAAATAAGATCCTACTTGGCAGTGCTTCTCCTGTCAATT  
CCAGGCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTNATTNATGTTTCCCTTGG  
CTGNGACTGGNTGGGCAGCATGCAGCTCTGATTAAAGAGGCATCTAGGGATTGTCAG  
GCACCCCTACAGGAAGGCCTGCCATGCTGTGGCAACTGTTCACTGGAGCAAGAAAGAGATC  
TCATAGGACGGAGGGGAAATGGTTCCCTCCAAGCTGGTCAGTGTGTTACTGCTTATC  
AGCTATTAGACATCTCCATGGTTCTCCATGAAACTCTGTGGTTCATCATTCTCTTAG  
TTGACCTGCACAGCTGGTTAGACCTAGATTAAACCTAAGGTAAGATGCTGGGTATAGAA  
CGCTAAGAATTTCACCCCAAGGACTCTGCTTCTTAAGCCCTCTGGCTTATGGTC  
TTCATTAAAAGTATAAGCCTAACTTGTGCTAGCCTAAGGAGAACCTTAACCACAAAG  
TTTTATCATTGAAGACAATATTGAACAAACCCCTATTTGTGGGATTGAGAAGGGTGAA  
TAGAGGCTTGAGACTTCCCTTGTGTGGTAGGACTGGAGGAGAAATCCCCTGGACTTCAC  
TAACCCCTCTGACATACTCCCCACACCCAGTTGATGGCTTCCGTAATAAAAGATTGGGATT  
TCCTTTG

## **FIGURE 76**

MAVLAPLIALVYSVPRLSRWLAQPYYLLSALLSAAFLLVRKLPPLCHGLPTQREDGNPCDFD  
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL  
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYNC  
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE  
ENVIREFNLNELYQRAKKLSKAGDNIPEEOPVASTPTVSDGENKKDK

**Signal sequence:**

amino acids 1-48

**Transmembrane domain:**

amino acids 111-125

**N-glycosylation site.**

amino acids 165-169, 185-189

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 154-158, 265-269

**Casein kinase II phosphorylation site.**

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

**N-myristoylation site.**

amino acids 188-194, 225-231

**Myb DNA-binding domain repeat signature 1.**

amino acids 244-253

## **FIGURE 77**

GGACAGCTCGCGGCCCCGAGAGCTCTAGCCGTCGAGGAGCTGCCTGGGACGTTGCCCTG  
GGGCCAGCCTGGCCGGTCACCCCTGGCATGAGGAGATGGCCTGTTGCTCCTGGTCCA  
TTGCTCCTGCTGCCCGCTCCTACGGACTGCCCTCTACAACGGCTCTACTACTCCAACAG  
CGCCAACGACCAGAACCTAGGCAACGGTCATGGCAAAGACCTCCTTAATGGAGTGAAGCTGG  
TGGTGGAGACACCCGAGGGAGACCCCTGTTCACCTACCAAGGGGCCAGTGTGATCCTGCCCTGC  
CGCTACCGCTACGAGCCGGCCTGGTCTCCCCGCGCGTGTGCGTGTCAAATGGTGAAGCT  
GTCGGAGAACGGGCCAGAGAAGGACGTGCTGGTGCCATGGGCTGAGGCACCGCTCCT  
TTGGGACTACCAAGGCCGCGTGCACCTGCGCAGGACAAAGAGCATGACGTCTGGAG  
ATCCAGGATCTCGGGCTGGAGGACTATGGCGTTACCGCTGTGAGGTCAATTGACGGCTGGA  
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGCGGGGTGTGGCTTTCTTACCAAGTCCCCA  
ACGGCGCTACCAGTTCAACTTCCACGAGGGCCAGCAGGTCTGTGCAGAGCAGGCTGCCGTG  
GTGGCCTCCTTGAGCAGCTCTCCGGCCTGGAGGAGGGCCTGGACTGGTGCAACGCCGG  
CTGGCTGCAGGATGCTACGGTGCAGTACCCCATCATGTTGCCCGGCAGCCCTGCCGTGG  
CAGGCCTGGCACCTGGCGTGCAGCTACGGCCCCGCCACGCCGCTGCACCGCTATGAT  
GTATTCTGCTTCGCTACTGCCCTCAAGGGCGGGTGTACTACCTGGAGCACCTGAGAAGCT  
GACGCTGACAGAGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATGCCAAGGTGGAC  
AGCTCTTGCCGCTGGAAAGTCCATGGCCTGGACCGCTGCAGCCTGGCTGGCAGAT  
GGCAGCGTCCGCTACCCGTGGTTCACCGCATCCTAACTGTGGCCCCCAGAGCCTGGGT  
CCGAAGCTTGCTTCCCGACCCGAGAGCCGTTGTACGGTGTACTGCTACCGCCAGC  
ACTAGGACTGGGCCTCCCTACTGGTGTTTATTGAGTGGT  
CGTTTCCCTGTGGTTGGAGCCATTTAACTGTTTATACTTCTCAATTAAATTCT  
TTAAACATTTTTACTATTTTGAAAGCAAACAGAACCCATGCCCTCCCTTGCTCCTG  
GATGCCCACTCCAGGAATCATGCTTGCTCCCTGGCCATTGCGGTTTGCGGCTCTG  
GAGGTTCCCCGCCATCCAGGCTGGTCTCCCTCCCTTAAGGAGGTTGGGCCAGAGTGGC  
GGTGGCCTGTCTAGAATGCCGCCGGAGTCCGGGATGGTGGGCACAGTTCTCCCTGCC  
CAGCCTGGGGAAAGAAGAGGCCCTGGGGCCTCCGGAGCTGGCTTGGCCTCTGCC  
CACCTCTACTTCTCTGTGAAGGCCGTGACCCAGTCTGCCACTGAGGGCTAGGGCTGGAA  
GCCAGTTCTAGGCTTCCAGGCGAAATCTGAGGGAGGAAGAAACTCCCTCCCCGTTCC  
TCCCTCTCGGTTCAAAGAATCTGTTGTCATTGTTCTCCTGTTCCCTGTGTGG  
GGAGGGGCCCTCAGGTGTGTACTTGAGCAATAATGGTGTATGACTGCCCTGCC  
AA  
AA

## **FIGURE 78**

MGLLLLVPLLLLPGSYGLPFYNGFYYSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ  
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD  
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVEELRGVVFPYQSPNGRYQFNFHEGQQ  
VCAEQAAVVASFEQLFRAWEELDWNCAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSGPR  
HRRLHRYDVFCFATALKGRVYYLEHPEKLTLTEAREACQEDDATIAKVGQLFAAWKFHGLDR  
CDAGWLADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

**Signal sequence:**

amino acids 1-17

**Casein kinase II phosphorylation site.**

amino acids 29-33, 53-57, 111-115, 278-282

**Tyrosine kinase phosphorylation site.**

amino acids 137-145

**N-myristoylation site.**

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

## **FIGURE 79**

## **FIGURE 80**

MMWRPSVLLLLLRLHGAQGKPSPDAGPHQGRVHQAPLSDAPHDDAHGNFQYDHEAFLGR  
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT  
YDTDGRVGWEELRNATYGHYAPGEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE  
ELTAFLHPEEFPHMRDIVAETLEDLDRNKGYVQVEEYIADLYSAEPGEEPAWVQTERQQ  
FRDFRDLNKDGHLDGSEVGHVLPPAQDQPLVEANHLLHESDTDKDGRSLKAEILGNWNMFV  
GSQATNYGEDLTRHHDEL

**Signal sequence:**

amino acids 1-20

**N-glycosylation site.**

amino acids 140-144

**Casein kinase II phosphorylation site.**

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,  
291-295, 298-302

**N-myristoylation site.**

amino acids 263-269, 311-317

**Endoplasmic reticulum targeting sequence.**

amino acids 325-330

## **FIGURE 81**

GGGCCTTGCCTCCGCACTCGGGCGCAGCCGGTGGATCTCGAGCAGGTGCGGAGCCCCGG  
GCGGCCGGCGCGGGTGCAGGGATCCCTGACGCCTCTGTCCTGTTCTTGTCGCTCCCAG  
CCTGTCGTCGTTGGCCCGCCCTCCCCCGCGGTGCGGGGTTGCACACCGATCCTG  
GGCTCGCTCGATTTGCCGCCAGGGCGCTCCAGACCTAGAGGGCGCTGGCCTGGAGCAG  
CGGGTCGTCGTTGTCCTCTCCTCTGCCGCCGGGATCCGAAGGGTGCGGGGCTCT  
GAGGAGGTGACGCCGGGCCTCCGCACCCTGCCCTGCCGCATTCTCCCTCTCCCAG  
GTGTGAGCAGCCTATCAGTACCAATGTCCGCAGCCTGGATCCCGCTCTGCCCTCGGTGTG  
TGTCTGCTGCTGCTGCCGGGCCGCGGGCAGCGAGGGAGCCGCTCCCATTGCTATCACATG  
TTTACCAAGGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCCTCTGCCAGGGGCTGCC  
CTCTGAGGAATTCTCTGTATGGGAACATAGTATATGCTCTGTATCAGCATATGTGGG  
GCTGCTGTCACAGGGAGTAATCAGCAAATCAGGGGACCTGTACGAGTCTATAGCCTACC  
TGGTCGAGAAAATATTCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTCTAGAT  
GGTCTGCTTCTTCACAGTAACTAAAGCAGGAAAGTAGTACACAGGAGGCCACAGGACAAGCA  
GTGTCCACAGCACATCCACCAACAGGTAACAGACTAAAGAAAACACCCGAGAAGAAAATGG  
CAATAAGATTGAAAGCAGACATTGCATTCTGATTGATGGAAGCTTAATATTGGCAGC  
GCCGATTTAATTACAGAAGAATTGTTGGAAAAGTGGCTCTAATGTTGGAAATTGAAACA  
GAAGGACCACATGTGGCCTTGTCAAGCCAGTGAACATCCAAATAGAATTACTTGAA  
AAACTTACATCAGCCAAAGATGTTGTTGCCATAAAGGAAGTAGGTTCAGAGGGGTA  
ATTCCAATACAGGAAAAGCCTTGAAGCATACTGCTCAGAAATTCTCACGGTAGATGCTGGA  
GTAAGAAAAGGGATCCCAAAGTGGTGGTATTATTGATGGTGGCCTCTGATGACAT  
CGAGGAAGCAGGCATTGTGGCCAGAGAGTTGGTGTCAATGTATTATAGTTCTGTGGCA  
AGCCTATCCCTGAAGAACCTGGGATGGTCAGGATGTCACATTGTTGACAAGGCTGCTGT  
CGGAATAATGGCTTCTCTTACACATGCCAACTGGTTGGCACCACAAAATACGTAAA  
GCCTCTGGTACAGAACAGCTGTGCACTCATGAACAAATGATGTGCAGCAAGACCTGTTATAACT  
CAGTGAACATTGCCCTTAATTGATGGCTCCAGCAGTGTGGAGATAGCAATTCCGCTC  
ATGCTGAATTGTTCCAACATAGCCAAGACTTTGAAATCTGGACATTGGTGCAGAT  
AGCTGCTGTACAGTTACTTATGATCAGCGCACGGAGTTCAAGTTCACTGACTATAGCACCA  
AAGAGAATGTCTCTAGCTGTCACTAGAAACATCCGCTATATGAGTGGTGGAACAGCTACTGGT  
GATGCCATTCTCACTGTTAGAAATGTGTTGGCCCTATAAGGGAGAGCCCCAACAGAA  
CTTCCTAGTAATTGTCACAGATGGCAGTCCTATGATGATGTCCAAGGCCCTGCAGCTGCTG  
CACATGATGCAGGAATCACTATCTCTGTGGTGTGGCTGGCACCTGGATGACCTG  
AAAGATATGGCTCTAAACGAAGGAGTCTCACGCTTCTCACAGAGAGTTCACAGGATT  
AGAACCAATTGTTCTGATGTCACTAGAGGATTGAGAGATTCTTAGAATCCCAGCAAAT  
AATGTAACATTGACAACAGAAAGAAAAGTACAAGGGATCCAGTGTGAAATTGTATT  
CTCATAATACTGAAATGCTTCTGATGACTAGAATCAGATACAAACTATTAAGTATGTCAAC  
AGCCATTAGGCAAATAAGCACTCCTTAAAGCCGCTGCCCTGTGTTACAATTACAGTGT  
ACTTGTTAAAACACTGCTGAGGCTTCATAATCATGGCTTCTAGAAACTCAGGAAAGAGGA  
GATAATGTGGATTAAAACCTTAAGAGTTCTAACCATGCCTACTAAATGTACAGATATGCAAA  
TTCCATAGCTCAATAAGAATCTGATACTTAGACCAAAAAAA

## **FIGURE 82**

MSAAWIPALGLGVCLLLPGPAGSEAAPIAITCFTRGLDIRKEKADVLCPGGCPLEEFSVY  
GNIVYASVSSICGAAVHRGVISNSGGPVRYSLPGRENYSSVDANGIQSQMLSRWSASFTVT  
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIQRRFNLQKN  
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLKNTSAKDVLFAIKEVGFRGGNSNTGKAL  
KHTAQKFFTVDAGVRKGIPKVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELG  
MVQDVTFVDKAVCRNNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI  
DGSSSGDSNFRLMLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLAVI  
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAHDAGITI  
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

**Signal sequence:**

amino acids 1-24

**N-glycosylation site.**

amino acids 100-104, 221-225

**Casein kinase II phosphorylation site.**

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,  
425-429, 478-482, 528-532

**N-myristoylation site.**

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,  
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

**Amidation site.**

amino acids 145-149

## **FIGURE 83**

CGCCCGCGCTCCGCACCCGGCCCACCGCGCCGCTCCGCATCTGCACCCGAGCCC  
GGCGGCCTCCGGGGAGCAGCAGATCCAGTCGGGCCCGCAGCGCAACTCGGTCCAGTCG  
GGCGGGCGCTCGGGCGCAGAGCGGATGCAGCGGCTGGGCCACCTGCTGTGCCTGC  
TGCTGGCGCGCGGTCCCCACGGCCCCCGCGCTCGACGGCGACCTCGGCTCAGTC  
AAGCCCAGCCGGCTCTCAGCTACCCGAGGAGGCCACCTCAATGAGATGTTCCGCGA  
GGTTGAGGAAGTGGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGG  
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTACCTCCCAGCTAT  
ACAATGAGACCAACACAGACAGAAGGTTGAAATAATACCACATGTGCACCGAGAAAT  
TCACAAGATAACCAACAACCAGACTGGACAAATGGTCTTTCAGAGACAGTTATCACATCTG  
TGGGAGACGAAGAAGGAGCAAGGAGCCACGAGTCATCATCGACGAGGACTGTGGGCCAGC  
ATGTAAGTGCCTTGCAGCTTCCAGTACACCTGCCAGCCATGCCGGGCCAGAGGATGCT  
CTGCACCCGGGACAGTGAGTGCTGTGGAGACCAGCTGTGTCTGGGGTCACTGCACCAAAA  
TGGCCACCAGGGGAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGCTG  
TGCTGTGCCTTCCAGAGAGGCCGCTGTTCCCTGTGTGACACCCCTGCCCGTGGAGGGCGA  
GCTTGCCATGACCCGCCAGCCGGCTCTGGACCTCATCACCTGGAGCTAGAGCCTGATG  
GAGCCTGGACCGATGCCCTGTGCCAGTGGCCTCCTCTGCCAGCCCCACAGCCACAGCCTG  
GTGTATGTGCAAGCCGACCTCGTGGGGAGCCGTGACCAAGATGGGAGATCCTGCTGCC  
CAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTTATGGAGGAGGTGCCAGGAGCTGG  
AGGACCTGGAGAGGGAGCCTGACTGAAGAGATGGCGCTGGGGAGCCTGCCGCTGCCGCT  
GCACTGCTGGGAGGGAGAGATTTAGATCTGGACCAAGGCTGTGGTAGATGTGCAATAGAA  
ATAGCTAATTATTCCCCAGGTGTGCTTAGGCGTGGCTGACCAGGCTTCTTACA  
TCTTCTTCCCAGTAAGTTCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTGTCAGC  
TCCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGCTTGGAGAGTCAGGCAGGGTTAAC  
TGCAGGAGCAGTTGCCACCCCTGTCCAGATTATTGGCTGCTTGCCTCTACCAGTGGCAG  
ACAGCCGTTGTTCTACATGGCTTGATAATTGTTGAGGGAGGAGATGAAACAATGTGG  
AGTCTCCCTCTGATTGGTTGGGAAATGTGGAGAAGAGTGCCTGCTTGCAAACATCAA  
CCTGGAAAAATGCAACAAATGAATTTCACGCAGTTCTTCCATGGCATAGGTAAGCTG  
TGCCTTCAGCTGTTGCAAGATGAAATGTTCTGTTACCCCTGCATTACATGTGTTATTCA  
AGCAGTGTGCTCAGCTCCTACCTCTGTGCCAGGGCAGCATTTCATATCCAAGATCAATT  
CCTCTCTCAGCACAGCCTGGGGAGGGGTCAATTGTTCTCCTCGTCATCAGGGATCTCAGAG  
GCTCAGAGACTGCAAGCTGCTGCCAAGTCACACAGCTAGTGAAGACCAGAGCAGTTCAT  
CTGGTTGTGACTCTAACGCTCAGTGCTCTCCACTACCCACACCAGCCTGGTGCCACCAA  
AAGTGTCCCCAAAAGGAAGGAGAATGGGATTTCCTGAGGCATGCACATCTGGAATTAAG  
GTCAAACATAATTCTCACATCCCTCTAAAGTAAACTACTGTTAGGAACAGCAGTGTCTCAC  
AGTGTGGGGCAGCGTCTTCTAATGAAGACAATGATATTGACACTGTCCCTTTGGCAGT  
TGCATTAGTAACCTTGAAAGGTATATGACTGAGCGTAGCATACAGGTTAACCTGCAGAAACA  
GTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTGCAAACATCAATTAGCAGCAAC  
TGAAGACAATTATCAACCAACACGTGGAGAAAATCAAACCGAGCAGGGCTGTGAAACATGGTT  
GTAATATGCGACTGCGAACACTGAACACTCAGCCACTCCACAAATGATGTTTCAGGTGTCA  
TGGACTGTTGCCACCATGTATTCCAGAGTTCTTAAAGTTAAAGTTGACATGATTGTA  
TAAGCATGCTTCTTGAGTTAAATTATGTATAAACATAAGTGCATTAGAAATCAAGC  
ATAAATCACTCAACTGCAAAAAAAAAAAAAAA

## **FIGURE 84**

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ  
HKLRSAVEEMEAEAAAAKASSEVNLANLPPSYHNETNTDKVGNNTIHVHREIHKITNNQTG  
QMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRQMLCTRSECCG  
DQLCVWGHCTKMATRGSGNTICDNQRDCQPGLCCAFQRGLFPVCTPLPVEGELCHDPASRL  
LDLITWELEPDGALDRPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV  
GSFMEEVHQELEDLERSLTEEMALGEPAAAAALLGEEI

**Signal sequence:**

amino acids 1-19

**N-glycosylation site.**

amino acids 96-100, 106-110, 121-125, 204-208

**Casein kinase II phosphorylation site.**

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,  
327-331

**N-myristoylation site.**

amino acids 202-208, 217-223

**Amidation site.**

amino acids 140-144

## **FIGURE 85**

## **FIGURE 86**

MRLLVAPLLLAWVAGATAATPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDNDLFLTA  
VPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARCDFHALPQLLSLHL  
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLSNLLRAIDSRWFE  
MLPNLEILMIGGNKVDAILDMDNFRPLANLRSVLVLAGMNLREISDYALEGLQSLSFYDNO  
LARVPRRALEQVPGLKFLDLNKNPLQRVPGDFANMLHLKELGLNNMEELVSIDKFALVNLP  
ELTKLDITNNPRLSFIHPRAFHLPQMETLMLNNNALSHQQTVESLPNLQEVGLHGNPIR  
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHCLPLISPRSFPPSLQ  
VASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVYPEGTLELRRVTAAEAGLYT  
CVAQNLVGADTKTVVVGRALLQPGRDEQGLELRVQETHPYHILLSWTPPNTVSTNLTW  
SSASSLRGQQGATALARLPRGTHSYNITRLLQATEYWAQAFADAHTQLACWARTKEATS  
CHRALGDRPGLIAILALAVLLAAGLAHLGTQPRKGVGRRPLPPAWAFWGWSAPSVRVV  
SAPIVLPWNPGRKLPRSSEGETLLPPLSQNS

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 629-648

**N-glycosylation site.**

amino acids 94-98, 381-385, 555-559, 583-587

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 485-489

**Casein kinase II phosphorylation site.**

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,  
243-247, 313-317, 488-492, 700-704

**Tyrosine kinase phosphorylation site.**

amino acids 532-540

**N-myristoylation site.**

amino acids 15-21, 493-499, 566-572

**Amidation site.**

amino acids 470-474, 660-664, 692-696

## **FIGURE 87**

GCAAGCCAAGGCCGCTGTTGAGAAGGTGAAGAAGTCCGGACCCATGTGGAGGAGGGGACATTGTGTACCGCCT  
CTACATGCGGCAGACCATCATCAAGGTGATCAAGTTCATCTCATCATCTGCTACACCGTCTACTACGTGCACAA  
CATCAAGTTCGACCGTGGACTGCACCGTGGACATTGAGAGCTGACGGGCTACCGCACCTACCGCTGTGCCAACCC  
CCTGGGCCACACTCTTCAGATCCTGGCGCTCTTCTACATCAGCCTAGTCATCTCTACGGCCTCATCTGCATGTA  
CACACTGTGGTGGATGCTACGGCGCTCCCTCAAGAAGTACTCGTTGAGTCGATCCGTGAGGAGAGCAGCTACAG  
CGACATCCCCGACGTCAAGAACGACTTCGCTTCTCATGCTGCACCTCATGACCAATAACGACCCGCTCTACTCCAA  
GCGCTTCGCCGCTTCTCTGCGAGGTGAGTGAGAACAGCTGCGGCAGCTGAACCTCAACAACAGTAGTGGACGCT  
GGACAAGCTCCGGCAGCGGCTCACCAAGAACGCGCAGGACAAGCTGGAGCTGCACCTGTCAGTGGCAT  
CCCTGACACTGTGTTGACTGGTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCCGACCGTGACCATCCCCGCC  
CAGCATTGCCAGCTCACGGGCCTCAAGGAGCTGAGGCTTACACACAGCGGCCAAGATGAGCAGCTGCCACAGTGGTAC  
GGCCTTCCTGCGCGAGAACCTGCGGGCGCTGCACATCAAGTTCACCGACATCAAGGAGATCCCCTGTTGAGCTA  
TAGCCCTGAAGACACTGGAGGAGCTGACCTGACGGGCAACTGAGCGGGAGAACACCGCTACATGTCATCGA  
CGGGCTCGGGAGCTCAAACGCCCTCAAGGTGCTGGCGCTCAAGAGCAACCTAACGCAAGCTGCCACAGTGGTAC  
AGATGTGGCGTGCACCTGCGAGACTGTCCATCAACAAATGAGGGCAGCAAGCTCATCGTCTCAACAGCCTCAA  
GAAGATGGCGAACCTGACTGAGCTGGAGCTGATCCGCTGCGACCTGGAGCGCATCCCCACTCCATCTTCAGCCT  
CCACAAACCTGCAAGGAGATTGACCTCAAGGACAACACCTCAAGAACCCATCGAGGAGATCATCAGCTTCCAGCACCT  
GCACCGCCTCACCTGCCCTAACGCTGTTACAACCACATGCCCTACATCCCCATCCAGATCGGCAACCTCACCAA  
CCTGGAGCGCCTTACCTGAACCGCAACAAGATCGAGAAGATCCCCACCCAGCTCTTCTACTGCCGCAAGCTGCG  
CTACCTGGACCTCAGCCACAACAAACCTGACCTTCTCCCTGCCGACATCGGCCCTCTGCGAGAACCTCCAGAACCT  
AGCCATCACGGCCAACCGGATCGAGACGCTCCCTCCGGAGCTTCCAGTGCCGGAAGCTGCGGGCCCTGACCT  
GGGCAACAACGTGCTGCAGTCAGTCCAGGGTGGGCGAGCTGACCAACCTGACGCAAGCTGCGAGATCGAGCTGCGGG  
CAACCGGCTGGAGTGCCTGCCGTGGAGCTGGCGAGTGCCCAGTGCTCAAGCGCAGCGGCTTGGTGGAGGA  
GGACCTGTTCAACACACTGCCACCCGAGGTGAAGGAGCGGCTGTGGAGGGCTGACAAGGAGCAGGCCAGAGCAG  
GCCGGGCCAGCACAGCAAGCAGCAGGACCGCTGCCAGTCTCAGGCCGGAGGGCAGGCCAGTCTCTCCAG  
AACTCCCGGACAGCCAGGACAGCCTCGGGCTGGCAGGAGCCTGGGCCGTTGTGAGTCAGGCCAGAGCGAGA  
GGACAGTATCTGTGGGGCTGGCCCTTTCTCCCTCTGAGACTCACGTCCCCCAGGGCAAGTGTGTTGGAGGAG  
AGCAAGTCTCAAGAGCGCAGTATTGATAATCAGGGTCTCCTCCCTGGAGGCCAGCTCTGCCCTGGGCTGAG  
CTGCCACCAGAGGTCTGGGACCCCTCACTTTAGTTCTGGTATTATTCTCCATCTCCACCTCCTCATCC  
AGATAATATACATTCCAAGAAAGTTCAGCCAGATGGAAGGTGTTCAGGGAAAGGTGGCTGCCCTTTCCCC  
TTGTCTTATTAGCGATGCCGCCGGCATTTAACACCCACCTGGACTTCAGCAGAGTGGTCCGGGGCAACCCAG  
CCATGGGACGGTCACCCAGCAGTGCGGGCTGGCTCTGGCTGCCGTCCAGGGAGAGCAGGCCCTCCAGCTGGA  
AAGGCAGGCCTGGAGCTTGCTCTCAGTTTGTGGCAGTTTAGTTTTGTGTTTTTTTTAAATCAA  
AAACAATTTTTAAAGCTTGAAGGGATGGTTGGGTTATTAAAAGAAAAAAACTTAAAAAAA  
AAAAGACACTAACGGCCAGTGAGTTGGAGTCAGGGCAGGGTGGCAGTTCCCTGAGCAAGCAGCCAGACGT  
TGAACGTGTTCTTCCCTGGGCCAGGGTGCAGGGTGTCTTCCGGATCTGGTGTGACCTGGTCCAGGAGTT  
CTATTGTTCTGGGAGGGAGGTTTTGTGTTGGGTTTTGGTGTCTTGTGTTCTTCTCC  
ATGTGTCTTGGCAGGCACTATTCTGTGGCTGTCGGCCAGAGGAATGTTCTGGAGCTGCCAACGGAGGGAGGAG  
ACTCGGGTTGGCTAATCCCCGATGAACGGTGCCTCACCTCCCTCCTGTCCTGCCCTGCCCTCTCCA  
CGCACAGTGTAAAGGAGCCAAGAGGAGCCACTTCGCCAGACTTGTGTTCCCCACCTCTGCCATGGGTGTGT  
CCAGTGCCACCGCTGGCTCCGCTGCTTCCATCAGCCCTGTCGCCACCTGGCTCTCATGAAGAGCAGACACTTA  
GAGGCTGGTGGGAATGGGAGGTGCGCCCTGGAGGGCAGGCAGGGTCCAGGCCGTTCCCTGGCG  
CTGGAGTGACACAGCCCAGTCGGCACCTGGTGGCTGGAGGCCAACCTGCTTGTGTTAGATCACTCGGGTCCCCACCTT  
AGAAGGGTCCCCGCCCTAGATCAATCACGTGGACACTAAGGCACAGTTTAGAGTCCTTGTCTTAATGATTATGT  
CCATCCGTCTGTCGGTCCATTGTGTTCTGCGTGTCAATTGGATATAATCCTCAGAAATAATGCACACTAG  
CCTCTGACAACCATGAAGCAAAAATCGTTACATGTGGGTCTGAACCTGTAGACTCGGTACAGTATCAAATAAA  
ATCTATAACAGAAAAAAAAAAAAAA

## **FIGURE 88**

MRQTIIKVIKFILIIICYTVYYVHNIKFVDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI  
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK  
RFAVFLSEVSENKLRLQNLNNNEWTLDKLQRQLTKNAQDKLELHLFMLSGIPDTVFDLVELEV  
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLRENLRALHIKFTDIKEIPLWI  
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI  
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHISIFSLHNLQEIDLKDNNLKTIEEIISFQ  
HLHRLTCLKLWYNHIAYIPIQIGNLTNERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT  
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRALHLGNNVLQSLPSRVGELETNLTQIE  
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

**Transmembrane domain:**

amino acids 51-75 (type II)

**N-glycosylation site.**

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 85-89

**Casein kinase II phosphorylation site.**

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,  
398-402, 493-497

**N-myristoylation site.**

amino acids 173-179, 261-267, 395-401, 441-447

## **FIGURE 89**

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCCTCTCCC GT  
CCCGCGGTGGTTGCTGCTGCCGTGCTGGCCTGAACGCAGGAGCTGTCAATTGACT  
GGCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC TACATG  
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCAT  
GTGGCTTCAGGGCGGTCCAGGC GGTCTAGCACTGGATTGGAAACTTGAGGAATTGGC  
CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATT  
GTGGATAATCCCGTGGGCACTGGGTTCA GTTATGTGAATGGTAGTGTCCTATGCCAAGGA  
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGAACCTCTCAGTTGCCACAAAG  
AATTCCAGACAGTTCCATTCTACATTTCTCAGAGTCCTATGGAGGAAAATGGCAGCTGGC  
ATTGGTCTAGAGCTTTATAAGGCCATT CAGCGAGGGACC ATCAAGTGCAACTTGCGGGGGT  
TGCCTGGGTGATT CCTGGATCTCCCCTGTTGATT CGGTGCTCTCCTGGGGACCTTACCTGT  
ACAGCATGTCTCTCGAAGACAAAGGTCTGGCAGAGGTGTCAAGGTTGCAGAGCAAGTA  
CTGAATGCCGTAAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT  
GATCATTGAACAGAACACAGATGGGTGAACCTCTATAACATCTTA ACTAAAAGCACTCCA  
CGTCTACAATGGAGTCGAGTCTAGAATT CACACAGAGCCACCTAGTTGTCTTGT CAGCGC  
CACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAA  
GCTCAAATTATT CCTGAGGATCAATCCTGGGAGGCCAGGCTACCAACGTCTTGTGAACA  
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC  
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATA ACCATGGGT CAGGAGGCCTG  
GGTGC GGAAACTGAAGTGGCCAGAACTGCCTAAATT CAGTCAGCTGAAGT GGAAGGCCCTGT  
ACAGTGACCC TAAATCTTGGAAACATCTGCTTTGTCAAGT CCTAC AAGAACCTTGCTTT  
TACTGGATTCTGAAAGCTGGTCAATGGTTCTCTGACCAAGGGACATGGCTCTGAAGAT  
GATGAGACTGGT GACTCAGCAAGAATAGGATGGATGGGCTGGAGATGAGCTGGTTGGC  
CTGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGGCCATTCTCCCTGTATCT  
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAAGCTCTGCAGAGGATAAAATCATTGTCTCT  
GGAGGCAATTGGAAATTATTCTGCTTCTTAAAAAAACCTAAGATTTTAAAAAATTGAT  
TTGTTTGATCAAAATAAGGATGATAATAGATATTAA

## FIGURE 90

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEWDYVTVRKDAYMFWWLYYATNSC  
KNFSELPLVMWLQGGPGGSSTGFGNFEIGPLSDLKPRKTTWLQAASLLFVDNPVGTGFSY  
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR  
GTIKCNFAGVALGDSWISPVDVLSWGPYLYSMSLLEDKGGLAEVSKVAEQVLNAVNKGLYRE  
ATELGKAEMIIIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDALS  
QLMNGPIRKKLKIIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL  
IVDTMGQEAWRKLKWPELPKFSQLWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP  
SDQGDMALKMMRLVTQQE

**Signal sequence:**

amino acids 1-25

**N-glycosylation site.**

amino acids 64-68, 126-130, 362-366

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 101-105

**Casein kinase II phosphorylation site.**

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

**N-myristoylation site.**

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,  
187-193, 195-201, 331-337, 332-338, 360-366

## FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGCGCGCGCGGGCGCTGCTGCTGGCGCTGCTGGCT  
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCCGTATCAGGACCATGCGGCCGA  
CGGGTCATCACGTGCGCATCGTGGGTGGAGAGGACGCCAACTCGGCGTTGGCGTGGCA  
GGGGAGCCTGCGCTGTGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG  
CACTCACGGCGCGCACTGCTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGTGGATG  
GTCCAGTTGCCAGCTGACTTCCATGCCATCCTCTGGAGCCTGCAGGCCTACTACACCCG  
TTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGAATTCACCTATGACATTG  
CCTTGGTGAAGCTGCTGCACCTGTCACCTACACTAAACACATCCAGCCCCTGTCTCCAG  
GCCTCCACATTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGTACATCAA  
AGAGGATGAGGCACTGCCATCTCCCCACACCCCTCCAGGAAGTTCAGGTGCCATATAACA  
ACTCTATGTGCAACCACCTCTCCTCAAGTACAGTTCCGCAAGGACATCTTGGAGACATG  
GTTTGTGCTGCCAACGCCAACGGCGGGAGGATGCCCTGCTCGGTGACTCAGGTGGACCCCT  
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG  
GTCGGCCAATCGGCCGGTGTACACCAATATCAGCCACCCTTGAGTGGATCCAGAAG  
CTGATGGCCCAGAGTGGCATGTCCCAGCCAGACCCCTCCTGGCCACTACTCTTTCCCTCT  
TCTCTGGCTCTCCACTCCTGGGCCGGTCTGAGCCTACCTGAGCCATGCAGCCTGGGC  
CACTGCCAAGTCAGGCCCTGGTTCTCTGTCTTGGTAATAAACACATTCCAGTTGA  
TGCCTTGCAGGGCATTCTCAAAAAAAAAAAAAAAA

## **FIGURE 92**

MGARGALLLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRLW  
DSHVCGVSSLSHRWALTAAHCFETYSSDLSDPSGMVQFGQLTSMPSFWSLQAYYTRYFVSNI  
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP  
SPHTLQEJVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKNG  
LWYQIGVVSWVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL  
LGPV

**Signal sequence:**

amino acids 1-18

**N-glycosylation site.**

amino acids 167-171, 200-204, 273-277

**Casein kinase II phosphorylation site.**

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

**N-myristoylation site.**

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,  
259-265, 269-275

**Amidation site.**

amino acids 33-37

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 252-263,

**Serine proteases, trypsin family, histidine active site.**

amino acids 78-84

## **FIGURE 93**

CCACCGCGTCCGGACGCGTGGGAAGGGCAGAATGGGACTCCAAGCCTGCCTCTAGGGCT  
CTTGCCCTCATCCTCTGGCAAATGCAGTTACAGCCCCGGAGCCGACCAGCGGAGGACGC  
TGCCCCCAGGCTGGGTGTCCTGGCCGTGCGGACCCCTGAGGAAGAGCTGAGTCTCACCTT  
GCCCTGAGACAGCAGAAATGTGAAAGACTCTCGAGCTGGTGCAGGCTGTGCGGATCCCAG  
CTCTCCTCAATACGAAAATACCTGACCCCTAGAGAATGTGGCTGATCTGGTGAGGCCATCCC  
CACTGACCCCTCCACACGGTGCAAAATGGCTCTGGCAGCCGGAGCCCAGAAGTGCCATTCT  
GTGATCACACAGGACTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC  
TGGGGCTGAGTTCATCACTATGTGGGAGGACCTACGGAAACCCATGTTGTAAGGTCCCCAC  
ATCCCTACCAGCTTCCACAGGCCCTGGCCCCCATGTGGACTTTGTGGGGACTGCACCGT  
TTTCCCCAACATCATCCCTGAGGCAACGTCCTGAGCCGAGGTGACAGGGACTGTAGGCCT  
GCATCTGGGGTAACCCCCCTGTGATCCGTAAGCATAACAATTGACCTACAAGACGTGG  
GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCAGTTCCCTGGAGCAGTATTCCATGAC  
TCAGACCTGGCTCAGTTCATGCGCTCTCGGTGGCAACATTGACATCAGGCATCAGTAGC  
CCGTGTGGTTGGACAAACAGGGCCGGGCCGGCCGGGATTGAGGCCAGTCTAGATGTGCAGT  
ACCTGATGAGTGTGGTGCACATCTCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG  
GGACAGGAGCCCTTCCTGCAGTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT  
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCCTACATCCAGCAGGTCA  
ACACTGAGCTCATGAAGGCTGCCCTGGGTCTCACCTGCTCTGCCCTCAGGTGACAGT  
GGGGCCGGGTGGTCTGCTCTGGAAGACACCAGTTCCGCCCTACCTTCCCTGCCCTCCAG  
CCCCTATGTCACCACAGTGGGAGGCACATCCTCCAGGAACCTTCCATCACAAATGAAA  
TTGTTGACTATATCAGTGGTGGCTTCAGCAATGTGTTCCACGGCCTTCATACCAGGAG  
GAAGCTGTAACGAAGTCTGAGCTCTAGCCCCACCTGCCACCATCCAGTTACTTCAATGC  
CAGTGGCCGTGCCTACCCAGATGTGGCTGCACTTCTGATGGCTACTGGTGGTCAGCAACA  
GAGTGCCCATTCATGGGTGTCCGGAACCTCGGCCCTACTCCAGTGTGTTGGGGATCCTA  
TCCTGATCATGAGCACAGGATCCTTAGTGGCCGCCCTCTGGCTTCTCAACCCAAG  
GCTCTACCAGCAGCATGGGCAGGTCTTTGATGTAACCCGTGGCTGCCATGAGTCCTGTC  
TGGATGAAAGAGGTAGAGGGCCAGGGTTCTGCTCTGGCTGGGATCTGTAACAGGC  
TGGGGAACACCAACTTCCAGCTTGTAAGACTCTACTCAACCCCTGACCCCTTCTATC  
AGGAGAGATGGCTGTCCCCTGCCCTGAAGCTGGCAGTTCACTCCCTTATTCTGCCCTGTTG  
GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCCTGAAA  
TGCTGTGAGCTTGACTTCACTCCAAACCCCTACCATGCTCCATCATACTCAGGTCTCCCTACT  
CCTGCCCTAGATTCTCAATAAGATGCTGAACCTAGCATTTTGAAATGCCCTCTCCCTCCGC  
ATCTCATTTCTCTTCAATCAGGCTTCCAAAGGGTTGTATAACAGACTCTGTGCACTA  
TTTCACTTGATATTCACTCCCAATTCACTGCAAGGAGACCTACTGTCACCGTTACTCT  
TTCCTACCCCTGACATCCAGAAACAATGGCCTCCAGTGCATACTTCTCAATCTTGCTTATG  
GCCTTCCATCATAGTGCCCACCTCCCTCTTACTTAGCTTCAAGGTCTTAACCTCTTG  
ACTACTCTTGCTTCCCTCTCATCAATTCTGCTTCTCATGGAATGCTGACCTTCATTGC  
TCCATTGAGATTGGCTCTCAGTTACTCATTGCCCCGGAAACAAATCACTGACA  
TCTACAACCATTACCATCTCACTAAATAAGACTTTCTATCCAATAATGATTGATAACCTAAA  
TGTAAAAAA

## **FIGURE 94**

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGVSLGRADPEEELSLTFALRQQNVERLS  
ELVQAVSDPSSPQYGKYLTLENVALVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL  
SIRQAELLPGAEFHYYVGGPTETHVVRSPHPYQLPQALAPHVDFVGLHRFPPTSSLRQRP  
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG  
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMSAGANISTWVYSSPGRHEGQEPFLQWLML  
LSNESALPHVHTVSYGDDEDSISAYIQRVNTELMKAARGLTLLFASGDGAGCWSVSGRH  
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP  
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG  
RPPLGFLNPRLYQQHGAGLFDVTRGCHESDLDEEVEGQGFCSGPFWDPVTGWGTPTSQLC

**Signal sequence:**

amino acids 1-16

**N-glycosylation site.**

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

**Glycosaminoglycan attachment site.**

amino acids 361-365, 408-412, 538-542

**Casein kinase II phosphorylation site.**

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

**N-myristoylation site.**

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,  
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,  
521-527, 533-539, 549-555

## **FIGURE 95**

GCCGCGCGCTCTCTCCGGCCCCACACCTGTCTGAGCGCGCAGCGAGCCGCGGCCGGC  
GGGCTGCTCGCGCGAACAGTGCTCGGCATGGCAGGGATTCCAGGGCTCCTCTTCTC  
TTCTTCTGCTCTGTGCTGTTGGCAAGTGAGCCCTACAGTGCCCCCTGGAAACCCACTTG  
GCCTGCATAACGCCCTCCCTGTCGCTTGCCCCAGTCTACCCCTCAATTAGCCAAGCCAGACT  
TTGGAGCCGAAGCAAATTAGAAGTATCTTCTCATGTGGACCCAGTGTCAAGGGAACT  
CCACTGCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTCTATGCCAATGG  
CAGCCGCACAGAGACGCAGGTGGCATCTACATCCTCAGCAGTAGTGGAGATGGGGCCAAAC  
ACCGAGACTCAGGGCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTATGGCTATGACAGC  
AGGTTCAGCATTGGAGGACTTCCTGCTCAACTACCCTTCTCAACATCAGTGAAGTT  
ATCCACGGGCTGCACCGCACCCGGTGGCAGAGAACGATGTCCCTCACAGCTGCCACTGCA  
TACACGATGGAAAAACCTATGTGAAAGGAACCCAGAACGCTTCAGCCATGCCGAGCAGATGAA  
AAGTTAAAGATGGTGGTCGAGGGGCCAACGACTCCACTTCAGCCATGCCGAGCAGATGAA  
ATTCAGTGGATCCGGGTGAAACGCACCCATGTGCCAAGGGTTGGATCAAGGGCAATGCCA  
ATGACATCGGCATGGATTATGATTATGCCCTCTGGAACTCAAAAAGCCCCACAAGAGAAAA  
TTTATGAAGATTGGGGTGAGCCCTCTGCTAAGCAGCTGCCAGGGGCCAGGGTCTGGGTCTAT  
TGGTTATGACAATGACCGACCAGGAATTGGTGTATCGCTCTGTGACGTCAAAGACGAGA  
CCTATGACTTGTCTACCAGCAATGCGATGCCAGCCAGGGCCAGGGTCTGGGTCTAT  
GTGAGGATGTGGAAGAGACAGCAGCAGAACGAGCAGGAAATTATTGGCATTTCAGG  
GCACCAAGTGGGTGGACATGAATGGTCCCCACAGGATTCAACGTGGCTGTCAGAACACTC  
CTCTCAAATATGCCAGATTGCTATTGGATTAAAGGAAACTACCTGGATTGTAGGGAGGG  
TGACACAGTGGTCCCTCTGGCAGCAATTAGGGCTTCATGTTCTATTAGGAGAGGCC  
AAATTGTTTTGTCAATTGGCGTGCACACGTGTGTGTGTGTGTGTGTAAAGGTGT  
CTTATAATCTTTACCTATTCTTACAATTGCAAGATGACTGGCTTACTATTGAAAATG  
GTTTGTGTATCATATCATATCATTAAGCAGTTGAAGGCATACTTTGCATAGAAATAA  
AAAAAAACTGATTGGGGCAATGAGGAATATTGACAATTAGTTAATCTTCACGTTTGT  
CAAACTTGATTTCATCTGAACCTGTTCAAAGATTATTAATATTAAATATTGGCATA  
CAAGAGATATGAAAAAAAAAAAAAA

0 9 8 7 6 5 4 3 2 1

## **FIGURE 96**

MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLQSTLNLA  
KPDGFGEAKLEVS  
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDGS  
SGKS  
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTA  
AHCIHDGKTYVK  
TQKLRVGFLKPKFKDGGRGANDSTS  
SAMPEQMKFQWIRVKRTHVPKGWI  
KGANDIGMDYDYA  
LLELKKPHKRKFMKIGVSPPAKQLPGGR  
IHFGSGYDNDRPGNLVYRFCDVKDETYD  
LQQCD  
AQPGASGSGVYVRMWKRQQQKWERK  
IIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYW  
IKGNYLDCREG

**Signal sequence:**

amino acids 1-19

**N-glycosylation site.**

amino acids 93-97, 207-211

**Glycosaminoglycan attachment site.**

amino acids 109-113, 316-320

**Casein kinase II phosphorylation site.**

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

**N-myristoylation site.**

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

**Serine proteases, trypsin family, histidine active site.**

amino acids 171-177

## **FIGURE 97**

GCATCGCCCTGGTCTCTCGAGCCTGCTGCCGTCCCCCCCCACAGCCATGGTGGTTT  
CTGGAGCGCCCCCAGCCCTGGGTGGGGCTGTCTCGCACCTCACCTCCCTGCTGCTGCTG  
GCGTCGACAGCCATCCTCAATGCGGCCAGGATAACCTGTTCCCCAGCCTGTGGGAAGCCCCA  
GCAGCTGAACCGGGTTGTGGCGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA  
GCATCCAGAAGAATGGGACCCACCAC TGCGCAGGTTCTTGCTCACCA GCGCTGGGTGATC  
ACTGCTGCCACTGTTCAAGGACAACCTGAACAAACCACACCTGTTCTTGCTGCTGGG  
GGCCTGGCAGCTGGGAACCCCTGGCTCTGGTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGC  
CCCACCCCTGTGATTCTGGAAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCGAG  
CGCTCCATACAGTTCTCAGAGCGGGCCTGCCCATCTGCCTACCTGATGCCTCTATCCACCT  
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTTCCCTTGC  
CCCACCCCTCAGACCCCTGCAGAACGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT  
CTGTACTGGCGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGCGCGCTACTT  
GGAGGGGGAGCGGGATGCTGTCTGGCGACTCCGGGGCCCCCTCATGTGCCAGGTGGACG  
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGCGAGGGCTGTGCCAGCGAACAGGCC  
GGGGTCTACATCAGCCTCTTGCGCACCGCTCTGGGTGGAGAACGATCGTCAAGGGGTGCA  
GCTCCCGGGCGCGCTCAGGGGGTGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGCCG  
CCGCGCGCTCCTAGGGCGCAGCGGACCGGGCTCGGATCTGAAAGGCGCCAGATCCACA  
TCTGGATCTGGATCTGCGCGGCCCTCGGCGGTTCCCCCGCCGTAAATAGGCTCATCTACC  
TCTACCTCTGGGGGCCGGACGGCTGCTGCGGAAGGAAACCCCTCCCCGACCGCCGAC  
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCCGCCAACGGCCTCATGTCCCCGCCAC  
GACTTCCGGCCCCGCCCGGGCCCCAGCGCTTTGTGTATATAAATGTTAATGATTTTAT  
AGGTATTTGTAACCCCTGCCACATATCTTATTATTCTCCAATTCAATAATTATTATT  
CTCCAAAAAAA

## **FIGURE 98**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318  
><subunit 1 of 1, 317 aa, 1 stop  
><MW: 33732, pI: 7.90, NX(S/T): 1  
MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARI PVPPACGKPQQLNRVVGGEDSTDSEWP  
WIVSIQKNGTHHCAGSLLTSRWVITAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVA  
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDG  
VPLPHPQTLQKLKVPIIDSEVC SHLYWRGAGQGPITEDMLCAGYLEGERDACLGDGGPLMC  
QVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSGQ  
SGAAARS

**Signal sequence:**

amino acids 1-32

**N-glycosylation site.**

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

**Glycosaminoglycan attachment site.**

amino acids 826-830

**Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

**Tyrosine kinase phosphorylation site.**

amino acids 607-615

**N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879

## **FIGURE 99**

GACGGCTGGCCACCATGCACGGCTCTGCAGTTCTGATGCTTCTGCTGCCGCTACTGCTA  
CTGCTGGTGGCCACCACAGGCCCGTTGGAGCCCTCACAGATGAGGAGAACGTTGATGGT  
GGAGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGA  
GATGGGACGAGGAGCTGGCCGCTTCGCCAAGGCCTACGCACGGCAGTGCCTGTGGGCCAC  
AACAAAGGAGCGCGGGCGCCGCGCGAGAAATCTGTTGCCATCACAGACGAGGGCATGGACGT  
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAAACCTCAGGCCGCCACCT  
GCAGCCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGCCAAGACAGAGAGGATC  
GGCTGTGGTCCCACCTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT  
GGTGTGCAACTATGAGCCTCCGGGAACGTGAAGGGAAACGCCCTACCAGGAGGGACTC  
CGTGCCTCCAAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC  
CCGGAAGATGCTCAGGATTGCCCTACCTGGTAAC TGAGGCCCATCCTCCGGCGACTGA  
AGCATCAGACTCTAGGAAAATGGGTACTCCTTCCCTAGCAACGGGATTCCGGCTTCT  
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCGCCTGCTGTGAAACCCAGGCC  
CCAACCTCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTGCGTAAC  
AACTGAGGTCCCTCATTGGCAGCTCACAGCCTGCCCTGGATGAGGAGCCAGTTA  
CCTTCCCCAAATCGACCCATGTTCTATCCAAAATCAGCAGACAAAGTGACAGACAAAACA  
AAAGTGCCCTCTAGGAGCCCAGAGAACTCTCTGGACCCCAAGATGTCCTGACAGGGCAAG  
GGAACCTCCTACCCATGCCAGGAGGCTGAGGCTGAGGCTGAGTTGCCCTCCAGTG  
AGGTCTTGGCCTCAGTTTCCAGGCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC  
CACACGGGGCACACCTCCTCCAAGTCCCTGCCAATTCCCCAATACCTCTGCCACCGCTAA  
TGCCACGGGTGGCGTGCCTGGCTCTGAGTCGCTGCCAGGTGCAGAGGCCCTGACA  
AGCCTAGCGTTGTGTCAGGGCTGAACCTGGCCCTGGTCACTGTGAGGGCCCTCCTGGGA  
CTACTGCTCCTGCCTCCTCTGGTGTGGCTGGAATCTTCTTGAATGGATACCAACTCAAAGGG  
TGAAGAGGTAGCTGTCCTCTGTCACTTCCCCACCCCTGCCCCAGCCCTAAACAAGATA  
CTTCTTGGTTAAGGCCCTCGGAAGGGAAAGGCTACGGGCATGTGCCTCATCACACCATCC  
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCCTGAGGACTGCACACC  
GGGCCACACCTCTCCTGCCCTCCCTGAGTCCTGGGGTGGGAGGATTGAGGGAGCT  
CACTGCCTACCTGGCCTGGGCTGTCTGCCACACAGCATGTGCCTCTCCCTGAGTGCCTG  
TGTAGCTGGGATGGGATTCCCTAGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGTTTC  
TTTGAATGGGGAGGCAGGGACGGAAAGGAAAGTAACCTGACTCTCCAATAAAACCT  
GTCCAACCTGTGAAA

## **FIGURE 100**

MHGSCSFLMLLLPLLLLLVATTGPVGALTDEEKRLMVELHNLYRAQVSPTASDMLHMRWDEE  
LAAFAKAYARQCVGHNKERGRRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ  
MCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQC  
PSGYHCKNSLCEPIGSPEDAQDLPYLVTEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEV  
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAHLPSLDEEPVTFPKS  
THVPIPKSADKVTDKTKVPSRSPENSMDPKMSLTGARELLPHAQEEAEAEELPPSEVLAS  
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVV  
SGLNSGPGHVWGPLLGLLLLPLVLAGIF

**Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 114-118, 403-407, 409-413

**Glycosaminoglycan attachment site.**

amino acids 439-443

**Casein kinase II phosphorylation site.**

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

**N-myristoylation site.**

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,  
250-256

**Amidation site.**

amino acids 82-86, 172-176

**Peroxidases proximal heme-ligand signature.**

amino acids 287-298

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.**

amino acids 127-138

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.**

amino acids 160-172

## **FIGURE 101**

GTAACGTAGGCTTTCAATTGGAGCCCCCTAACAGAACCGTCATTCTCCAAGTTATGGTGGACGT  
ACTCTGTTGTTCTCCCTGCTTGCTTTCACATTAGCAGACCGACTAAGTCACAACAGATTATCTTCAT  
CAAGGCAAGTCCATGAGCCACCTCAAAGCCTCGAGAAACTGAACAACAATGAATTGGAGACCATTCC  
AAATCTGGGACCAAGTCTGGCAAATATTACACTCTCTCCTGGCTGGAAACAGGATTGTGAAATACCTCC  
ACATCTGAAAGAGTTCACTGCCCTGAAACTTTGGACCTTAGCAGCAACAATATTTCAGAGCTCCAAACTGCATT  
TCCAGCCCTACAGCTAAATATCTGTATCTAACAGCAACCGAGTCACATCAATGGAACCTGGTATTGGACAA  
TTTGGCCAACACACTCCTGTGAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTAAACT  
GCCCAACTGCAACATCTGAATTGAACCGAAACAAGATTAAGATGGACTGACATTCCAAGGCCTGG  
TGCTCTGAAGTCTGAAATGCAAGGAAACTTATGGATGGAGCTTTTGGGGCTGAGCAA  
CATGGAAATTTCAGCTGGACATAACAACCTAACAGAGATTACCAAAGGCTGGCTTACGGCTTGCTGATGCT  
GCAGGAACCTCATCTCAGCCAAATGCCATCAACAGGATCAGCCCTGATGCCCTGGAGTTCTGCCAGAAGCTCAG  
TGAGCTGGACCTAATTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCTGGCTAAGCTTACTAAATAC  
ACTGCACATTGGAAACAACAGAGTCAGCTACATTGCTGATTGTGCTTCCGGGGCTTCCAGTTAAAGACTTT  
GGATCTGAAGAACATGAAATTCTGGACTATTGAAGACATGAATGGTCTTCTGGAGTGATGAAACTGAG  
GCGACTGATACTCCAAGGAAATCGGATCCGTTCTATTACTAAAAAGCTTCACTGGTTGGATGATGGAGCA  
TCTAGACCTGAGTGAACCGCAATCATGTCTTACAAGGCAATGCATTTCACAAATGAAGAAACTGCAACAATT  
GCATTAAATACATCAAGCCTTTGTGCATTGCCAGCTAAATGGCTCCACAGTGGTGGCGAAAACAACCTT  
TCAGAGCTTGAAATGCCAGTTGTGCCATCCTCAGCTGCTAAAGGAAGAACGATTTTGCTGTTAGGCCAGA  
TGGCTTGTGTGATGATTTCCAAACCCCAGATCACGGTTAGCCAGAACACAGTCGGAATAAAAGGTT  
CAATTGAGTTCATCTGCTCAGCTGCCAGCAGTGAATCCCAATGACTTTGCTTGGAAAAAAAGACAATGA  
ACTACTGCATGATGCTGAAATGGAAATTATGCACACCTCCGGGCCAAGGTGGCAGGTGATGGAGTATACCAC  
CATCCTCGGCTGCGCAGGTGAAATTGCCAGTGAGGGAAATATCAGTGTGTCATCTCAATCACTTGGTC  
ATCCTACTCTGCAAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTCACCAAGACCCCCATGGATCTCACC  
CCGAGCTGGGGCCATGGCACGCTTGGAGTGTGCTGTGGGACCCAGCCCCCAGATAGCCTGGCAGAAGGA  
TGGGGCACAGACTTCCAGCTGCACGGAGAGACGCATGATGTGATGCCAGGTGATGGTCTTATCGT  
GGATGTGAAGATAGAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTCAGCAAATGC  
AACTCTGACTGTCTAGAAACACCATATTGGCGGCCACTGTTGGACCGAACGTGTAACCAAGGGAGAAACAGC  
CGTCCTACAGTGCATTGCTGGAGGAAGGCCCTCCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTGGT  
AACCGAGAGGCACTTTTGTCAGGCAATCAGCTCTGATTATTGTGGACTCAGATGTCAGTGTGATCTGGAA  
ATACACATGTGAGATGCTAACACCCCTGGCACTGAGAGGAAACCTGGCCTCAGTGTGATCCCCACTCCAAC  
CTGCGACTCCCCCTCAGATGACAGCCCCATGTTAGACGATGACGGATGGGCACTGTGGTGTGATCATAGC  
CGTGGTTGCTGTGGTGGCACGTCACTCGTGTGGTGTGATCATATACACACAAGGGGAGGAATGAAGA  
TTGCAGCATTACCAACACAGATGAGACCAACTGCCAGCAGATATTCTAGTTATGTGTCATCTCAGGGAAACGTT  
AGCTGACAGGCAGGATGGGTACGTGCTTCAGAAAGTGGAGGCCACCCAGTTGTCACATCTCAGGGTGTGG  
ATTTTCTTACACACATGACAGTAGTGGACCTGCCATTGACAATAGCAGTGAAGCTGATGTGAAAGCTGC  
CACAGATCTGTTCTTGTCCGTTTGGGATCCACAGGCCCTATGTATTGAAAGGGAAATGTGATGGCTCAGA  
TCCTTTGAAACATATCATACAGGTTGCACTCCTGACCCAGAACACAGTTTATGGACCACTATGAGCCCAGTT  
CATAAAGAAAAAGGAGTGTACCCATGTCATCCTTCAGAAGAACCTCGCAACGGAGCTCAGTAATATATC  
GTGGCTTCACATGTGAGGAAGCTACTTAACACTAGTTACTCTCACAAATGAAGGACCTGGAATGAAAATCTGT  
TCTAAACAAGTCTCTTGTGAAAGCTCATTCTCCAGACTTGGACTCTGGTCAAGGATTCAGTAACTTCTCATGGG  
TACCTTGAAAGCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTTGGACAGCCATCAGATTGTCAGCC  
AAGAGCCTTTATGTGAAAGCTCATTCTCCAGACTTGGACTCTGGTCAAGGAGATGGAAAGAAAGGAC  
AGATTTCAGGAAGAAAATCACATTGTACCTTAAACAGACTTTAGAAAACAGTCCAAATTTCAGTC  
TTATGACTTGGACACATAGACTGAATGAGACCAAAGGAAAAGCTTAACATACACTACCTCAAGTGAACCTT  
AAAGAGAGAGAACTTATGTTAAATGGAGTTATGAATTAAAGGATAAAATGCTTTATTTATACAGAT  
GAACCAAAATTACACAAAGTTATGAAATTTTATACTGGGAATGATGCTCATATAAGAACACCTTTAAACTA  
TTTTTTAACTTGTGTTATGCAAAAAGTATCTACGTAATTAAATGATATAAAATCATGATTATTTATGTATT  
TTATAATGCCAGATTCTTTATGAAAATGAGTTACTAAAGCATTAAATAACCTGCCCTGTACCAATT  
TTAAATAGAAGTTACTCATTATATTGACATTATTTAATAAAATGTGTCATTTGAA

## **FIGURE 102**

MVDVLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLQLSQLREVKLNNNELETIPNLGPVSAN  
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEP  
GYFDNLANTLLVLKLNRRNRIASIPPKMFKLQPQLQHLELRNKIKNVGLTFQGLGALKSLKM  
QRNGVTKLMGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWE  
FCQKLSELDLTFNHLRSRLLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRLSSLKTLDLKNN  
ISWTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQ  
MKKLQQLHLNTSSLLCDCQLKWLPOWVAENNQSFVNASCAPQLLKGRSIFAVSPDFVCD  
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKDNELLHDAEMENYAHLRQAQG  
GEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGA  
MARLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCAQN  
SAGSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKNWTKDDSPVVTER  
HFFAAGNQLLIIVDSDVSDAGKYTCEMSNTLGTERGNVRLSVIPTPTCDSPQMTAPSLLDDG  
WATVGVIIIAVVCCVVGTSLVVVIIYHTRRRNEDCSITNTDETNLPADIPSYLSSQGTTLAD  
RQDGYSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLCFLCPFLGSTGP  
MYLKGNVYGSDPFETYHTGCSPDPRTVLMHYEPSYIKKKECYPCHPSEESCERSFSNISW  
PSHVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDA  
YSSFGQPSDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQS  
YDLDT

**Signal sequence:**

amino acids 1-19

**Transmembrane domain:**

amino acids 746-765

**N-glycosylation site.**

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

**Glycosaminoglycan attachment site.**

amino acids 826-830

**Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

**Tyrosine kinase phosphorylation site.**

amino acids 607-615

**N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879

## **FIGURE 103**

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTGGTGGTGGCTTGGGTGCCTGCAAAATG  
AAGGATGCAGGACGCAGCTTCTCCTGGAACCGAACGCAATGGATAAAACTGATTGTGCAAGAGAGAAGAAC  
GAAGCTTTCTTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAA  
TAAACCAGAGTTAGACCCCGGGGGTGGTGTCTGACATAAATAATCTTAAAGCAGCTGTTCCCTCC  
CCACCCCCAAAAAAAGGATGATTGAAAGAAGAACCGAGGATTCAAAGAAAAAGTATGTTCATTTCTC  
TATAAAGGAGAAAGTGAAGCCAAGGGAGATATTGGAATGAAAAGTTGGGGCTTTTAGTAAAGTAAAGAACT  
GGTGTGGTGGTGTCTTCTTGAATTCCCACAAAGAGGAGAGGAAATTAAATAACATCTGCAAAGAAA  
TTTCAGAGAAGAAAAGTGAACCGCGCAGATTGAGGCATTGATTGGGGAGAGAAACACAGCAGAGCACAGTTGGA  
TTTGCCATGTTGACTAAAATTGACGGATAATTGCACTGGATTCTCTTCTTCAACCTCCATTTTTAAAT  
TTTTATTCCCTTTGGTATCAAGATCATGCCTTCTTCTTCAACACCCTGGATTCCATCTGGATGTTGCT  
GTGATCAGTCTGAAATACAACGTGTTGAATTCCAGAAGGACCAACACAGATAAATTGATGTTGAAACAAGAT  
GACCTTACATCCACAGCAGATAATGATAGGTCTAGGTTAACAGGGCCATTGGACCTGCCCTCTGTGCTGGTGC  
GCTGGCTCTCAACTTCTGGTGGCTGGTCTGGTGGCTCAGACACTGCCCTCTGTGCTGGTGC  
CCAGTTCAAGGTGATTGTTGGAAAAACCTCGTGGAGGTTCCGGATGGCATCTCCACCAACACAGGCT  
GCTGAACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCTCAAGCACTTGAGGACTTGGAAATCCT  
ACAGTTGAGTAGGAACCATATCAGAACCAATTGAAATTGGGGCTTCAATGGTCTGGGAACCTCAACACTCTGGA  
ACTCTTGACAATCGCTTACTACCATCCGAATGGAGCTTGTATCTGTCTAAACTGAAGGAGCTCTGGTT  
GCGAAACAACCCATTGAAAGCATCCCTCTTACAGAATTCCCTTGGCGCGACTAGACTTAGG  
GGAATTGAAAAGACTTTCATACATCTCAGAAGGTGCTTGAAGGTCTGCCAACCTGAGGTTATTGAACCTTGC  
CATGTGCAACCTCGGGAAATCCCTAACCTCACACCGCTCATAAAACATAGATGAGCTGGATCTTCTGGGAATCA  
TTTATCTGCCATCAGGCCTGGCTCTTCCAGGGTTGATGCACCTTCAAAACTGTGGATGATACTGCCCAGAT  
TCAAGTGAACGGAATGCCCTTGACAACCTCAGTCACTAGTGGAGATCAACCTGGCACACAATACTAAC  
ATTACTGCCTCATGACCTCTCACTCCCTTGACATCATCTAGAGCGGATACATTACATACAACCCCTGGAACTG  
TAACTGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCTCGAACACAGCTTGTGCCCCGGTG  
TAACACTCCTCCAATCTAAAGGGGAGGTACATTGGAGAGCTGACCAGAATTACTTCACATGCTATGCTCCGGT  
GATTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGCAGCTGAGCTGAAATGTCGGGCTCCACATC  
CTGACATCTGTATCTGGATTACTCTCAAATGGAACACTCATGACACATGGGGCTACAAAGTGCAGTAGCTGT  
GCTCAGTGTGGTACGTTAAATTTCACAAATGTAACCTGTGCAAGATAAGGCATGTACACATGTATGGTGGTAA  
TTCCGGTGGGAATACTACTGCTTCAGGACCCCTGAATGTTACTGTCAGGAAACACTACTCCTTCTTACTTTTC  
AACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACGGACACAGATAACAATGTGGGCCCCACTCC  
AGTGGTCGACTGGAGACCAATGTGACCACTCTCTCACACCACAGAGCACAAGGTGAGAGAAAAACCTT  
CACCATCCCAGTGAATATAAACAGTGGGATCCCAGGAATTGATGAGGTCTGAGACAGACTACCAAAATCATCAT  
TGGGTGTTTGGCCATCACACTCATGGCTGAGCTGATGCTGGTCTTCAAGATGAGGAAGCAGCACCA  
TCGGCAAAACCATCACGCCAACAAAGGACTGTGAAATTATTAATGTGGATGAGATTACGGGAGACACACC  
CATGGAAAGCCACCTGCCATGCCTGCTATCGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTT  
CAACCACACAAACACAGTTAACACAATAATTCAATACACAGTTCACTGAGCTGATGAAACCGTTATTGATCCGAATGAA  
CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTTACAGAGTTACAAAAACAAACAAATCAAAAAAA  
GACAGTTATTAAAAATGACACAAATGACTGGGCTAAATCTACTGTTCAAAAGTGTCTTACAAAAAAACAA  
AAAAGAAAAGAATTATTATTAAAAATTCTATTGTGATCTAAAGCAGACAAAAA

## **FIGURE 104**

MLNKMTLHPQQIMIGPRFNRALFDPLLVVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKVIC  
VRKNLREVPDGISTNTRLLNLHENQIQIICKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA  
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS  
YISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKL  
WMIQSQIQVIERNADFNLQSLVEINLAHNNLTLLPHDLFTPPLHHLERIHLHHNPWCNC  
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLN  
TEGMAAE LKCRASTSLSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMV  
NSVGN TTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWE  
TTNVTTSLTPQ STRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRK  
QHHRQN HHAPTRTVEIINV DDEITGDTPMESHPMPAIEHEHLNHYNSYKSPFNHTT  
TVNTINSIHSS VHEPLLIRMSKDNVQETQI

**Signal sequence:**

amino acids 1-44

**Transmembrane domain:**

amino acids 523-543

**N-glycosylation site.**

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,  
442-446, 488-492, 606-610

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

**Casein kinase II phosphorylation site.**

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

**N-myristoylation site.**

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,  
391-397, 422-428, 433-439, 531-537

## **FIGURE 105**

AGCCGACGCTGCTCAAGCTGCAACTCTGTCAGTTGCAGTTGGCAGTTCTTCCCTCTGCTGTTGGGGCA  
TGAAAGGGCTTCGCCGCCGGAGTAAAAGAAGGAATTGACCAGGGCAGCGCAGGGAGGAGCGCAGCGACCGC  
GAGGGCGGGCGTGACCCCTCGGCTGAAAGTTGTGCCGGGCCCCGAGCGCGCAGGGCTGGAGCTTCGGGAG  
GACCTAGGCCGCTGGACCGCAGAGCCTCCGTGCGCGCAGGGCTGGGAGCTGGCTGCTGTGC  
GCGGTGCTGGGGCGCGTGGCGTCCGACAGCGCGGTGCGGGGAACTCGGGAGCCCTCTGGGTAGCGGCC  
GAGCGCCCAGGCCCACTACCTGCCGCTGCCCTGGGACCTGCTGGACTGCACTGTAAGCGGCTAGCGCTT  
CCCCAGCCACTCCCGTCTGGGTGCGCTGGACTTAAGTCACAACAGATTATCTTCATCAAGGCAAGTCC  
ATGAGCCACCTCAAAGCCTCGAGAAGTGAAGACTGAACAACAATGAATTGGAGAACATTCCAATCTGGGACCA  
GTCTCGGCAAATATTACACTTCTCTTGGCTGAAACAGGATTGTGAAATACTCCCTGAACATCTGAAAGAG  
TTTCAGTCCCTGAAACTTGGACCTTAGCAGCAACAATATTTCAGAGCTCCAAGTGCATTCCAGGCCACAG  
CTCAAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGGATTGGCAAAATTGGGCAACACA  
CTCCTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCCAAAGATGTTAAACTGCCCAACTGCAA  
CATCTGAATTGAAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCCTGGTGTCTGAAGTCT  
CTGAAAATGCAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTTGGGGCTGAGCAACATGGAATTGG  
CAGCTGGACCATAACACCTAACAGAGATTACCAAAGGCTGGCTTACGGCTTGTGATGCTGCAGGAACCTCAT  
CTCAGCCAAATGCCATCAACAGGATCAGCCCTGATGCCCTGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCA  
ACTTTCAATCACTTCAAGGTTAGATGATTCAAGCTTCCCTGGCCTAACGTTACTAAATACACTGCACATTGGG  
AACAAACAGAGTCAGCTACATTGCTGATTGTGCCCTCCGGGGCTTCCAGTTAAAGACTTGGATCTGAAGAAC  
AATGAAATTTCCTGGACTATTGAAGACATGAATGGTCTTCTCTGGGCTTGACAAACTGAGGCGACTGATACTC  
CAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTTCACTGGTTGGATGCAATTGGAGCATCTAGACCTGAGT  
GACAACGCAATCATGTCTTACAAGGCAATGCATTTCACAAATGAAGAAACTGCAACAATTGCATTAAATACA  
TCAAGCCTTTGTGCGATTGCCAGCTAAATGGCTCCCACAGTGGTGGCGGAAACAAACTTCAAGAGCTTGTA  
AATGCCAGTTGCCATCTCAGCTGCTAAAGGAAGAACGATTGGCTGTTAGCCAGATGGCTTGT  
GATGATTTCACAAACCCAGATCACGGTTCAGGCCAGAAACACAGTCGGCAATAAAGGTTCAATTGAGTTTC  
ATCTGCTCAGCTGCCAGCAGTCAGTCTCCCAATGACTTTGCTTGGAAAAAGACAATGAACACTGCACTGAT  
GCTGAAATGGAAAATTATGCAACACCTCCGGGCCAAGGTGGCAGGTGATGGAGTATACCAACCATCTTGGCTG  
CGCAGGGTGGAAATTGCCAGTGAGGGAAATATCAGTGTGTCATCTCCAATCAGTGTGTTCATCCTACTCTGTC  
AAAGCCAAGCTTACAGTAAATATGCTTCCCTATTCACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGCC  
ATGGCACGCTGGAGGTGTGCTGCTGGGGCACCCAGCCCCCAGATGCGTGGCAGAAGGATGGGGCACAGAC  
TTCCCAGCTGCACGGGAGAGACGCATGATGTGATGCCAGGGATGACGTGTTCTTATGTGGATGTGAAGATA  
GAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTGCAAGGAAGTATTCAAGCAATGCAACTCTGACTGTC  
CTAGAAACACCATCATTTGCCACTGTTGGACCGAACTGTAACCAAGGGAGAACAGCCGTCTACAGTGC  
ATTGCTGGAGGAAGGCCCTCCCCCTAAACTGAACTGGACCAAAGATGATGAGCCATTGGTGGTAACCGAGAGGCAC  
TTTTTGAGCAGGCAATCAGCTCTGATTATTGTGGACTCAGATGTCAGTGCTGGAAATACACATGTGAG  
ATGCTAACACCTTGGCACTGAGAGAGGAAACGTCAGGCCACTCCAAACCTGCACTCCCCT  
CAGATGACAGCCCCATCGTTAGACGATGACGGATGGGCACCTGTGGGTGCTGATCATAGCCGTGGTTGCTGT  
GTGGTGGCAGTCACTCGTGTGGTGTATCATACACACAAGCGGAGGAATGAAGATTGCAGCATTAC  
AACACAGATGAGACCAACTGCCAGAGATATTCTAGTTATTGTCTACAGGAAACGTTAGCTGACAGGAG  
GATGGTACGTTCTCAGAAAGTGGCAAGCCACCACTGTCACATCTCAGGTGCTGGATTTCCTTACCA  
CAACATGACAGTAGTGGCACCTGCCATATTGACAATAGCAGTCAGTGAGCTGCCACAGATCTGTC  
CTTGTGCGTTGGGATCCACAGGCCCTATGTTAGGGAAATGTGTATGGCTCAGATCTTGGAAACA  
TATCATACAGGTTGCAGTCCTGACCCAGAAACAGTTTAATGGACCACTATGAGCCAGTTACATAAAGAAAAG  
GAGTGTACCCATGTTCTCATCCTCAGAAGAACTCTGCAACGGAGCTTCAGTAATATATCCTGCGCTTCACAT  
GTGAGGAAGCTTAACACTAGTTACTCTCACAAATGAAGGACCTGGAAATGAAAATCTGTCATAAACAGTCC  
TCTTGTGTTTAATGGAGTTATGAATTAAAGGATAAAATGCTTATTTACAGATGAAACCAAAATTAC  
AAAAAGTTATGAAATTTTACTGGGAATGATGCTCATATAAGAATACCTTTAAACTATTTTAACTTTG  
TTTATGCAAAAAGTATCTACGTTAAATTAGTATGATATAATCATGATTATTTATGTATTTTATAATGCCAGA  
TTCTTTTATGGAAATGAGTTACTAAAGCATTAAATAACCTGCCCTGTGACCAATTAAATAGAAGTT  
ACTTCATTATATTGCACTTAAATTAAATGTGCAATTGAAAAA

## **FIGURE 106**

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAEERPCPTTCRCLGDILLDCSR  
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNELETIPNLGPVSANIT  
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGY  
FDNLANTLLVLKLNRNRISSAIPPKMFKLQPQLQHLELNRNKIKNVGGLTFQGLGALKSLKMQR  
NGVTKLMGAFWGLSNMEILQLDHNNLTEITKGWLGYGLLMLQELHLSQNAINRISPDAWEFC  
QKLSELDLTNFNHLRSRLLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRLGSSLKTLKLNNEIS  
WTIEDMNGAFSGLDKLRRLLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMK  
KLQQLHLNTSSLCDQLKWLPOWVAENNFQSFVNASCAPHQPLLKGRSIFAVSPDGVCDDF  
PKPQITVQPETQSAIKGSNLNFICSAASSSDSPMTFAWKKDNELLHDAEMENYAHLRAQGE  
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGAMA  
RLECAAVGHPPAQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA  
GSISANATLTVLETPSFLRPLLDRVTKGECVAVLQCIAGGSPPPKNWTKDDSPLVVTERHF  
FAAGNQLLIIVDSDVSDAGKYTCEMSNTLGTERGNVRSLVIPTPTCDSPQMTAPSLLDDGWA  
TVGVVIIAVVCCVVGTSLVVVVIYHTRRRNEDCSITNTDETNLPADIPSYLSQGTLADRO  
DGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGPMY  
LKGNVYGSDFPFETYHTGSPDPRTVLMHYEPSYIKKKECYPCHPSEESCERSFSNISWPS  
HVRKLLNTSYSHSNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDAYS  
SFGQPSDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEENHICTFKQTLNEYRTPNFQSYDLDT

**Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 808-828

**N-glycosylation site.**

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,  
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

**Glycosaminoglycan attachment site.**

amino acids 886-890

**Casein kinase II phosphorylation site.**

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,  
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,  
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,  
1073-1077, 1079-1083, 1081-1085

**Tyrosine kinase phosphorylation site.**

amino acids 667-675

**N-myristoylation site.**

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,  
513-519, 588-594, 672-678, 683-687, 774-780, 933-939

**Leucine zipper pattern.**

amino acids 58-80, 65-87

## **FIGURE 107**

CAAAACTTGCCTCGCGGAGAGCGCCCCAGCTTGAATTGAAGGAGCCCGAGCCCGGGAGCGCAGCTGAGAC  
TGGGGGAGCGCGTTGGGCCCTGTGGGCGCCGCTCGGCGCCGGGCGCAGCAGGAAGGGAGCTGTGGTCTGCC  
CTGCTCCACGAGGCGCCACTGGTGTGAACCGGGAGAGGCCCTGGGTGTCCTCCCCTATCCCTCCTTATATA  
GAAACCTTCCACACTGGGAAGGCAGCGGGAGGGCAGGGCTCATGGTGAGCAAGGAGGCCGGCTGATCTGCAG  
GCGCACAGCATTGGAGTTACAGATTTACAGATAACCAAATGGAAGGCAGAGGAGGCAGAACAGCCTGCCTGGT  
TCCATCAGCCCTGGGCCAGGCGCATCTGACTCGGCACCCCTGCAGGCACCATGGCCCAGAGGCCGGGTGCTGC  
TGCTCCTGCTGCTGCTGCCACAGCTGCACTGGGACCTGTGCTTGCGCTGAGGGCCCCAGGATTGGCGAA  
GTGGCGCCACAGCCTGAGCCCCGAAGAGAACGAATTGGGGAGGAGGAGGCCGGTGTGACTGAGCCCTGAGG  
AGCCCGGGCTGGCCAGCCGGTCAAGCTGCCCGAGACTGTGCTCTGGCCAGGAGGGCGTGTGACTGTG  
GCGGTATTGACCTGCGTGAAGTCCCGGGGACCTGCTGAGCACCCAACCACCTATCTCTGAGAACAAACCAGC  
TGGAAAAGATCTACCCCTGAGGAGCTCTCCCGCTGCACTGGAGACACTGAAACCTGCAAAACCGCCTGA  
CTTCCCAGGGCTCCAGAGAAGGCGTTGAGCATCTGACCAACCTCAATTACCTGTACTTGGCCAATAACAAGC  
TGACCTTGGCACCCGCTTCTGCCAACGCCCTGATCAGTGTGACTTGTGCTGCCAACATCTCACCAAGATCT  
ATGGGCTCACCTTGGCCAAGGCAAACCTTGAGGTCTGTGTACCTGACAACAACAAGCTGGCAGGCCGGG  
TGCCGGACAACATGTTCAACGGCTCCAGCAACGTCAGGTTCTCATCTGTCCAGCAACTTCTGCGCACGTGC  
CCAAGCACCTGCCCTGCCCTGTACAAGCTGACCTCAAGAACACAAGCTGGAGAAGATCCCCCGGGG  
TCAGCGAGCTGAGCAGCTGCGAGCTATACTGAGAACAAACTACCTGACTGAGCAGGGCCTGGACAACGAGA  
CCTTCTGGAAGCTCTCAGCCTGGAGTACCTGGATCTGTCCAGCAACAACCTGTCCTGGGCTCCAGCTGGGCTGC  
CGCGCAGCCTGGTGTGCTGCACTTGAGAAGAACGCCATCCGGAGCGTGGACCGGAATGTGCTGACCCCC  
GCAGCCTGGAGTACCTGCTGCTGCACAGCAACCAGCTGCGGGAGCAGGGCATCCACCCACTGGCCTTCCAGGG  
TCAAGCGGTTGCACACGGTGCACCTGTACAACAACGCGCTGGAGCGCGTGCCTGGCTGCC  
GCACCCCTCATGATCCTGCACAACCAGATCACAGCATTGGCGCGAAGACTTGGCACCACCTACTTCTGGAGG  
AGCTCAACCTCAGCTACAAACCGCATCACCGCCACAGGTGACCGCAGCCTCGCAAGCTGCGCTGCTGC  
GCTCGCTGGACCTGTCGGCAACCGGCTGCAACGCTGCCACCTGGGTGCTCGAAATGTCATGTGCTGAAGG  
TCAAGCGCAATGAGCTGGCTGCCCTGGCACAGGAGGGCGCTGGCGGGCATGGCTCAGCTGCGTGAGCTGTACCTCA  
CCAGCAACCGACTGCCAGCCGAGCCCTGGGCCCCCTGCTGGTGGACCTCGCCCATCTGAGCTGCTGGACA  
TCGCCGGGAATCAGCTCACAGAGATCCCCGAGGGCTCCCGAGTCACCTGAGTACCTGAGAACAACA  
AGATTAGTGCCTGGCCCAATGCCCTGCACTCCACGCCAACCTCAAGGGGATCTTCTCAGGTTAACAGC  
TGGCTGTGGCTCGTGGTGGACAGTGCCTCCGGAGGGCTGAAGGACCTGCAAGGCTTGGACATTGAAGG  
TAGAGTTGGTGAACATTCCAAGGACCGTGGCCCTTGGGAAGGAAAGAGGAGGAGGAGGAAGAGGAGGAGG  
AGGAAGAGGAAACAAGATAGTGACAAGGTGATGAGATGTGACCTAGGATGATGGACCGCCGACTCTTCTGC  
AGCACACGCTGTGCTGAGCCCCCACTCTGCCGTGTCACACAGACACACCCAGCTGCACACATGAGGCA  
TCCCACATGACACGGGCTGACACAGTCTCATATCCCCACCCCTGCCAGGGCTGCTCCACGCCAGACACATGC  
ACACACATCACACCCCTCAAACACCCAGCTCAGCCACACACA  
CCCCACTACCGCTGCCACGCCCTCTGAATCATGCAGGGAGGGCTGCCCTGGCACACACAGGCACCA  
TTCCTCCCCCTGTCGACATGTGTATGCGTATGCATACACACCACACACACATGCACAAGTCATGTGCGAA  
CAGCCCTCCAAAGCCTATGCCACAGACAGCTTGGCCAGCCAGAATCAGGCACTAGCAGCTGCCGTG  
GTCCATCTGTCGCTCCGTTCCCTGGAGAAGACACAAGGTATCCATGCTGTGGCCAGGTGCC  
GGAACTCACAAAGCTGGCTTTATTCCCTTCCATGCCATGGGACAGGAGCCTCAGGACTGCTGGCCTGG  
TGGCCACCCCTGCTCCAGGTGCTGGCAGTCACTCTGCTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA  
CAGGCACTTTCCAATGGGAAGGCCAGCTGGAGGCAGGATGGGAGAGGCCCTGGGTGCTGCTGGGCTTGGGG  
CAGGAGTGAAGCAGAGGTGATGGGCTGGCTGAGCCAGGGAGGAAGGAGCCAGCTGCACCTAGGAGACAC  
GTTCTCAGGCCCTGIGGGGAAGTTCGGGTGCCCTTATTCTTATTCTTAAGGAAAAAAATGATAAAA  
CTCAAAGCTGATTTCTGTTATAGAAAAACTAATAAAAGCATTATCCCTATCCCTGCAAAAAAA

## **FIGURE 108**

MEGEEAEQPAWFHQWPWRPGASDSAPPAGTMAQSRVLLLLLPPQLHLGPVLAVRAPGFGRS  
GGHSLSPPEENEFAEEEPLVLSPEEPGPAAVSCPDCACSQEGVVDCGGIDLREFPGDLP  
EHTNHLSLQNNQLEKIYPEELSRLHRLETNLQNNRLTSRGLPEKAFLTNLNLYLANNK  
LTLPAPRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV  
EVLIILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN  
ETFWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSVDANVLPIRSLEYLLLHSN  
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPRTLMILHNQITGIGREDFATTYF  
LEELNLSYNRITSQPVHRDAFRKLRLRSLDLSGNRLHTLPPGLPRNVHVLKVKRNEALAALA  
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL  
QNNKISAVPANAFDSTPNLKGIIFRFNKLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKD  
RGRLGKEKEEEEEEEEEEETR

**Signal sequence:**

amino acids 1-48

**N-glycosylation site.**

amino acids 243-247, 310-314, 328-332, 439-443

**Casein kinase II phosphorylation site.**

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

**N-myristoylation site.**

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,  
477-483, 498-502, 539-545, 548-554

**Leucine zipper pattern.**

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,  
535-557

## **FIGURE 109**

# **FIGURE 110**

MDFLLALVLVSSLYLQAAAEDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCOPVCQP  
RCKHGE CIGPNKCKCHPGYAGKTCNQDLNECGLKPRPC KHRCMNTYGSYKCYCLNGYMLMPD  
GSCSSALTCSMANCQYGCDVVKGQIRCQCPSPGLHLAPDGRTCDVDECATGRASCPRFQRC  
VNTFGSYICKCHKGFDL MYIGGKYQCHDIDECSLGQYQCSSFARCVNRGSYKCKCKEGYQG  
DGLTCVYIPKVMIEPSGPIHVPKGNGTILKGDTGNNNWIPDVGSTWWPPKTPYIPPIITNRP  
TSKPTTRPTPKPTPIPTPPPPPPLPTELRTPLPPTTPERPTTGLTTIAPA AASTPPGGITVDN  
RVQTDPQKPRGDVF SVLVHSCNF DHGLCGWI REKDNDLHWEPI RD PAGGQYLT VSAAKAPGG  
KAARLVLPLGRLMHSGDLCLSFRHKVTGLHS GTLQVFVRKHGAHGA ALWGRNGGHGW RQ TQI  
TLRGADIKSESQR

**Signal sequence:**

amino acids 1-17

**N-glycosylation site.**

amino acids 273-277

**Casein kinase II phosphorylation site.**

amino acids 166-170, 345-349

**Tyrosine kinase phosphorylation site.**

amino acids 199-206

**N-myristoylation site.**

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,  
421-427, 433-439, 462-468, 476-482

**Aspartic acid and asparagine hydroxylation site.**

amino acids 104-116, 186-198, 231-243

**Cell attachment sequence.**

amino acids 382-385

**EGF-like domain cysteine pattern signature.**

amino acids 75-87

## **FIGURE 111**

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTGCATTGCCCTTAGATTGTGA  
**AATGTGGCTCAAGGTCTTCACAAC**TTCCCTTGCACAGGGTGCCTGCTCGGGGCTGA  
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAAGGCCCTACCTACCCGTC  
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTGAGAGACCCA  
ACAATGCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTCTGACTTGGAAATACC  
AACACAAGTCACCATGATGCCACCAATGCATCTGCTTATCAACCCACTGCAGTTCCCT  
GATGAAGGCAATTACATCGTAAGGTCAACATTCAAGGAAATGGAACACTATCTGCCAGTC  
GAAGATAACAAGTCACGGTTGATGATCCTGTACAAAGCCAGTGGTGCAGATTCATCCTCCCT  
CTGGGGCTGAGTATGTGGGAACATGACCCCTGACATGCCATGTGGAAGGGGGCACTCGG  
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTC  
TCCCCAAAACAATACCTTCAATTGCTCCAGTAACCAAGGAAGACATTGGAATTACAGCT  
GCCTGGTGAGGAACCTGTCAAGTGAATTCTGATAAAGGGCTAAAAGTAGGGGAAGTGTACTGT  
TGACCTTGGAGAGGCCATCCTATTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT  
CCTGGATTAGGAGGACTGACAATACTACATATCATTAAGCATGGGCCTCGCTAGAAGTT  
GCATCTGAGAAAGTAGCCCAGAAGACAATGGACTATGTGTGCTGTGCTTACAACACATAAC  
CGGCAGGCAAGATGAAACTCATTCACAGTTATCATCACTCCGTAGGACTGGAGAAGCTG  
CACAGAAAGGAAAATCATTGTCAACCTTCAAGTATACTGGAATATCACTATTGATT  
ATATCCATGTGTTCTCTTCTATGGAAAAAATCAACCCATCAAAGTTATAAAACAGAA  
ACTAGAAGGCAGGCCAGAACAGAACATCAGGAAAGCTCAAACATTTCAGGCCATGAAGATG  
CTCTGGATGACTTCGGAATATATGAATTGTTGCTTCCAGATGTTCTGGTGTTCAGG  
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTTATGGGCAAGATTGCACAGTACAGT  
GTATGAAGTTATTCAAGCACATCCCTGCCAGCAGCAAGACCATTCAAGTTGAACTTCATGG  
GCTAAACAGTACATTGAGTGAAAATTCTGAAGAACATTAAAGGAAAACAGTGGAAAAGT  
ATATTAATCTGGAATCACTGAAGAACAGGACCAACACCTTACTCATTATTCTTACA  
TGCAGAACAGGATTATGCAAATTGAACTGCAGGTTTCAGCATATAACAAATGTCTT  
GTGCAACAGAAAACATGTTGGGAAATATTCCCTCAGTGGAGAGTCGTTCTCATGCTGACGG  
GGAGAACGAAAGTGACAGGGTTCTCATAAGTTGTATGAAATATCTACAAACCTCA  
ATTAGTTCTACTCTACACTTCACTATCATCAACACTGAGACTATCCTGTCACCTACAAA  
TGTGGAAACTTACATTGTTGATTTTCAGCAGACTTTGTTTATTAAATTGTTATTAGTG  
TTAAGAATGCTAAATTATGTTCAATTATTCCTATCTTCAAGTTGTATTTGACAA  
CAAAGTAATAAGGATGGTTGTCAAAAAACAAAACATGCCTCTTTTTCAATCACC  
AGTAGTATTGAGAAGACTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTGTTA  
TTTTTTCAAGGAAAGATGGATTCAAATAATTCTGTTTGTGTTAAAAAAAAAAAAAA

## **FIGURE 112**

MWLKVFTTFLSFATGACSGLKVTVPSPHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH  
TMPKYLLGSVNKSVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGLTLSASQ  
KIQVTVDPPVTKPQQIHPGSAVEYVGNMTLTCHEGGTRLAYQWLKNGRPVHTSSTYSFS  
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNNSDKGLKVGEVFTV  
DLGEAILFDCSADSHPPNTYSWIRTDNTTYIIKHGPRLEVASEKVAQKTMDYVCCAYNNIT  
GRQDETHFTVIITSVGLEKLAQKGKSLSPLASITGISLFLIISMCLLFLWKKYQPYKVIKQK  
LEGRPETEYRKAQTFSGHEDALDDFGIYEFPDVSGVSRIPSRSVPASDCVSGQDLHSTV  
YEVIOHIPAQQQDHPE

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 341-359

**N-glycosylation site.**

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,  
276-280, 308-312

**Casein kinase II phosphorylation site.**

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

**Tyrosine kinase phosphorylation site.**

amino acids 272-280

**N-myristoylation site.**

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,  
239-245

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## **FIGURE 113**

GCAAGCGGC~~GAAATGGCGCCCTCCGGGAGTCTTCAGTTCCCTGGCAGTCCTGGTGTGTT~~  
GCTTG~~GGGTGCTCCCTGGACGCACGGCGGCCAGCACGTTCCGTCATCACGGACGAGA~~  
ACTGGAGAGAAC~~TGCTGGAAGGAGACTGGATGATAGAATTATGCCCCGGTGCCTGCT~~  
TGTCAA~~AAATCTCAACCAGGAATGGAAAGTTGCTGAATGGGAGAAGATCTTGAGGTTAA~~  
TATTG~~CAGAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTATCATAACTGCTC~~  
TTC~~CTACTATTATCATTGTAAGATGGTGAATTAGGCCTATCAGGGCCAAGGACTAAG~~  
AAGGACTTC~~CATAAACTTATAAGTGATAAAGAGTGGAAAGAGTATTGAGCCCCTTCATCATG~~  
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTCAGCTATCTATGTGGA  
TCAGGACGTGCCATAACTACTTATTG~~AAGACCTTGGATTGCCAGTGTGGGATCATATACT~~  
GTTTG~~CCTTAGCAACTCTGTTCCGGACTGTTATTAGGACTCTGTATGATATTGTGGC~~  
AGATTG~~CCTTGTCCCTCAAAAAGGCCAGACCCACAGCCATACCCATACCCCTCAAAAAAAAT~~  
TATTATC~~AGAATCTGCACAACCTTGAAAAAAGTGGAGGAGGAACAAGAGGCCGATGAAGAA~~  
GATG~~TTCCAGAAGAAGACTGAAAGTAAAGAAGGAACAAACAAAGACTTCCACAGAATGC~~  
CAT~~AAGACAACGCTCTGGGCCATCATTGGCACAGATAATCCTAGTAAATTATAG~~  
TTATCTTA~~ATATTATGATTTGATAAAAACAGAAGATTGATCATTGTTGGTTGAAGTG~~  
AACTGT~~GACTTTTGAAATTGCAGGGTCAGTCTAGATTGTCATTAAATTGAAGAGTCTA~~  
CATT~~CAGAACATAAAAGCACTAGGTATACAAGTTGAAATTGATTTAACAGTATGATG~~  
GTT~~AAATAGTTCTAATTGAAAAATCGGCCAGCAATAAGATTATGTATATTGT~~  
TTAATA~~ATAACCTATTCAAGTCTGAGTTGAAAATTACATTCCCAAGTATTGATTCTGATTAT~~  
TGAGG~~TATTAGAAGATTATTAGAGAAAATTCTCATTTGATATAATTCTCTG~~  
TTCACT~~GTTGAAAAAGAAGATATTCCATAATGGGAAGTTGCCATTGCTCAAG~~  
AAATGT~~GTTTCAGTGACAATTCTGGTCTTTAGAGGTATATTCCAAAATTCTCTG~~  
ATTTT~~TAGTTATGCAACTAATAAAACTACCTTACATTAATTAAATTACAGTTCTACACA~~  
TGG~~TAATACAGGATATGCTACTGATTAGGAAGTTTAAGTTCATGGTATTCTTGATTC~~  
CAAC~~AAAGTTGATTCTCTGTATTCTTACTTACTATGGGTACATTTTATTGTT~~  
CAAATTGG~~GATAATTCTGGAAACATTTTATGTTAGTAAACAGTATTGTTGTT~~  
GTT~~CAAACGTTGAAAGTTACTGAGAGATCCATCAAATTGAACAATCTGTTGTAATTAAAATT~~  
TTGCC~~ACTTTTCAGATTTCATCATTCTGCTGAACCTCAACTGAAATTGTTTTTT~~  
TTCTT~~TTGGATGTAAGGTGAACATTCTGATTGTTCTGATGTGAAAAAGCCTGGTA~~  
TTTAC~~ATTGAAATTCAAAGAAGCTTAATATAAAAGTTGCATTCTACTCAGGAAAAG~~  
CAT~~CTTCTGTATATGCTTAAATGTATTGTCCTCATATACAGAAAGTTCTTAATTGAT~~  
TTTAC~~AGTCTGTAATGCTGATGTTAAAATAACATTATTATTTAAAGACAA~~  
ACT~~TCAATTATCCTGTTCTGACTGGTAATATTGTGTTGGGATTTCACAGGTAAA~~  
GTC~~CAGTAGGATGGAACATTAGTGTATTGTTACTCCTTAAAGAGCTAGAATACATAGTTT~~  
CAC~~CTTAAAGAAGGGGAAATCATAAATACAATGAATCAACTGACCATTACGTAGTAGAC~~  
AATT~~TCTGTAATGTCCTTCTTAGGCTCTGTTGCTGTGAATCCATTAGATTACAG~~  
TAT~~CGTAATATACAAGTTCTTAAAGCCCTCCTTCTGATGCTTAGAATTAAAATTGTA~~  
AAAGAG~~TTGGATGTAACTTGTGATGCCTTAGAAAAATATCCTAAGCACAAATAACCT~~  
TTCTAAC~~CCACTTCATTAAGCTGAAAAAAAAAAAAAA~~

## **FIGURE 114**

MAPSGSLAVPLAVLVLLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL  
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI  
NFISDKEWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL  
ATLFSGLLLGLCMIFVADCLCPSKRRPQPYPYPSKKLLSESAQPLKKVEEEQEADEEDVSE  
EEAESKEGTNKDFPQNAIRQRSLGPSLATDKS

**Signal sequence:**

amino acids 1-26

**Transmembrane domain:**

amino acids 182-201

**Casein kinase II phosphorylation site.**

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

**Tyrosine kinase phosphorylation site.**

amino acids 107-115

**N-myristoylation site.**

amino acids 20-26, 192-198

**Amidation site.**

amino acids 25-29

## **FIGURE 115**

GCGAGTGTCCAGCTGGAGACCCGTGATAATTGTTAACTAATTCAACAAACGGGACCCTT  
CTGTGTGCCAGAAACCGCAAGCAGTGTGCTAACCCAGTGGGACAGGCAGGATTGGAAGAGCGGG  
AAGTCCTGGCCCAGAGCAGTGTGACACTTCCCTCTGTGACCTGAAACTCTGGGTGTCTGC  
ATTGCTGATGGCCTGGTTGGTGTGAGCTGTGTCAGGGCAATTCTCACCTCTATTG  
GGCACATGACTGACCTGATTATGCAGAGAAAGAGCTGGTGAGTCTGTGAAAGAGTACATC  
CTTGTGGAGGAAGCCAAGCTTCCAAGATTAAGAGCTGGCCAACAAAATGGAAGCCTTGAC  
TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCCTACAAACTGG  
TGAAGCGGCTAACACACAGACTGGCCTGCGCTGGAGGACCTTGTCTGCAGGACTCAGCTGCA  
GGTTTTATGCCAACCTCTGTGCGAGCGGAGTTCTCCCCACTGATGAGGACGAGATAGG  
AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTCCA  
GAGGGGAACCTCCAGGAACCAAGTACCAAGGCAATGCTGAGTGTGGATGACTGCTTGGATG  
GGCCGCTCGGCCTACAATGAAGGGACTATTATCATACGGTGTGGATGGAGCAGGTGCT  
AAAGCAGCTTGATGCCGGGAGGAGGCCACCAACCAAGTCACAGGTGCTGGACTACCTCA  
GCTATGCTGCTTCCAGTTGGGTGATCTGCACCGTGCCTGGAGGCTCACCCGCCGCTGCTC  
TCCCTGACCAAGCCACGAGCTGGAGGAATCTCGGTACTTGAGCAGTTATTGGA  
GGAAGAGAGAGAAAAACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCCAGAAGGCA  
TCTATGAGAGGCCTGTGGACTACCTGCCTGAGAGGGATGTTACGAGAGCCTCTGCGTGGG  
GAGGGTGTCAAACGTACACCCGTAGACAGAAGAGGCTTCTGTAGGTACCAACATGGCAA  
CAGGGCCCCACAGCTGCTATTGCCCTTCAAAGAGGAGGACGAGTGGACAGCCGACA  
TCGTCAAGGTACTACGATGTCATGTGATGAGGAAATCGAGAGGATCAAGGAGATCGAAAAA  
CCTAAACTTGCACGAGCCACCGTCTGTGATCCCAAGACAGGAGTCCTCACTGCGCAGCTA  
CCGGGTTCCAAAGCTCTGGCTAGAGGAAGATGATGACCTGTTGTGGCCGAGTAAATC  
GTCGGATGCAGCATATCACAGGTTAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAAT  
TATGGAGTGGGAGGACAGTATGAACCGCACTCGACTTCTCTAGGCGACCTTGACAGCGG  
CCTAAAACAGAGGGAAATAGGTTAGCGACGTTCTTAACACATGAGTGTAGAAGCTG  
GTGGTGCACCGTCTCCCTGATCTGGGGCTGCAATTGGCTAAGAAGGGTACAGCTGTG  
TTCTGGTACAACCTCTGGAGGGAGGAAAGGTGACTACCGAACAGACATGCTGCTGCC  
TGTGCTTGTGGCTGCAAGTGGGTCTCCAATAAGTGGTCCATGAACGAGGACAGGAGTTCT  
TGAGACCTGTGGATCAACAGAAGTTGACTTGACATCCTTCTGCTCTCCCTCTGGTC  
CTTCAGCCCATGTCAACGTGACAGACACCTTGTATGTTCTTGTATGTTCTATCAGGCT  
GATTTTGAGGAAATGAATGTTGTCTGGAGCAGAGGGAGACCATACTAGGGCGACTCCTGT  
GTGACTGAAGTCCCAGCCCTTCCATTGAGCCTGTGCCATCCCTGGCCCAAGGCTAGGATCA  
AAGTGGCTGAGCAGAGTTAGCTGTCTAGCGCTAGCAAGGTGCTTGTACCTCAGGTGTT  
TTAGGTGTGAGATGTTCAAGTGAACCAAAGTTCTGATACCTGTTACATGTTGTTTAT  
GGCATTCTATCTATTGTGGCTTACCAAAAAATAAAATGTCCCTACCAGAAAAAA

## **FIGURE 116**

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWA  
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALEDLVLQDSAGFIANLSVQRQFFP  
TDEDEIGAAKALMRLQDTYRLDPGTISRGELPGTKYQAMLSVDDCFGMGRSAYNEGDYYHTV  
LWMEQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRAELTRRLLSLDPSHERAGGNLR  
YFEQLLEEEEREKTLTNQTEAELATPEGIYERPVDYLPERDVYESLCRGEGVKLTPRQKRLF  
CRYHHGNRAPQOLLIAPFKEEDEWDSPHIVRYYDVMSDEEIERIKEIAKPKLARATVRDPKTG  
VLTVASYRVSKSSWLEEDDPVVARVNRRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFRS  
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAIWPKKGTAVFWYNLLRSGEGDYR  
TRHAACPVLVGCKWVSNKFHERGQEFLRPCGSTEVD

**Signal sequence:**

amino acids 1-17

**N-glycosylation site.**

amino acids 115-119, 264-268

**Glycosaminoglycan attachment site.**

amino acids 490-494

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 477-481

**Casein kinase II phosphorylation site.**

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,  
346-350, 365-369, 385-389, 457-461, 530-534

**Tyrosine kinase phosphorylation site.**

amino acids 71-80, 489-496

**N-myristoylation site.**

amino acids 14-20, 131-137, 171-177, 446-452

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 8-19

**Leucine zipper pattern.**

amino acids 213-235

## FIGURE 117

GCAGTATTGAGTTTACTCCCTCTTTAGTGAAGACAGACCATAATCCAGTGTGAGTGAAATTGATTGT  
TTCATTTATTACCGTTGGCTGGGGTTAGTCCGACACCTTCACAGTGAAGAGCAGGCCAGAAGGAGTTGTGA  
AGACAGGACAATCTTCTGGGGATGCTGGCTTGAAGCCAGCAGGGCTTGCTCTGTCTTGGCTCATTGACCC  
CAGGTTCTCTGGTTAAACTGAAAGCCTACTACTGGCTGGCCATCAATCATTGATCCTTGAGGCTGTGCC  
CCTGGGGCACCCACCTGGCAGGGCTACCAATCGCACTGAGCTCCCTGTTGGCTCTGCTGCCAGCGCTTC  
CCCTCATCTTAGGGCTCTCTGGGGTGCAGCCTGAGCCTCTGCGGGTTCTGGATCCAGGGGAGGGAGAAG  
ATCCCTGTGTCGAGGCTGAGGGAGCCACAGAACATCCAGATTGAGAGCTGGCTAGACCAAAGTGAAG  
ATGAAGACTCTAAACCCCCGATTGTCCTACTACAGGGACCCAAACAAGCCCTACAAGAAGGTGCTCAGGACTC  
GGTACATCCAGACAGCAGCTGGCTCCGTGAGCGGTTGCTGGCTGACCTCCGAGCTACACTGTCCA  
CTTGGCCGTGGCTGTGAACCGTACGGTGGCCATCACTCCCTCGGTTACTCTACTTCACGGCAGGGGG  
CCCGGGCTCCAGCAGGGATGCAAGTGGTGTCTATGGGGATGAGCGCCGGCTGGCTATGTCAGAGACCCCTGC  
GCCACCTCACACACACTTGGGCCGACTACGACTGGTCTTCATCATGCAAGGATGACACATATGTCAGGCC  
CCGCCTGGCAGCCCTGCTGCCACCTCAGCATCAACCAAGACCTGACTTAAAGCCGGAGAGGAGTTCATIG  
GCGCAGGCAGCAGGCCGGTACTGTCACTGGGGCTTGCTACCTGTTGTCACGGAGTCTCTGCTTCGTCTGC  
GGCCACATCTGGATGGCTGCCAGGGACATTCTCAGTGGCCGCTTGACGAGTGGCTTGACGCTGCCATTG  
ACTCTCTGGCGTCTGGCTGTCACAGCACCAGGGCAGCAGTATGCTCATTTGAACGGCCAAAATAGGG  
ACCCCTGAGAAGGAAGGGAGCTGGCTTCCCTGAGTGCCITGCCGTGACCCCTGCTCCGAAGGTACCCCTATGT  
ACCGGCTCCACAAACGCTCAGCGCTCTGGAGTTGGAGGGCTTAAGTGAATAGAACAACTGCAAGGCTCAGA  
TCCGGAACCTGACCGTGTGACCCCCGAAGGGGAGGCAGGGCTGAGCTGGCCGGTTGGCTCCCTGCTCCTTCA  
CACACACACTCTGCTTTGAGGTGCTGGCTGGACTACTTCACAGACGACACACCTCTCCTGTGCAAGATGGGG  
CTCCAAGTGCCACTACAGGGGCTAGCAGGGCGACGTGGGTGATGCCGTGAGACTGCCCTGGAGCAGCTCA  
ATCGCGCTATCAGCCCCCCTGCCAGAACAGCAGGACTGCTCAACGGCTATCGCGCTTCGACCCAGCAC  
GGGGCATGGAGTACACCCCTGGACCTGCTGTTGAAATGTGTGACACAGCGTGGCACCGGGGGCCCTGGCTCGA  
GGGTCACTGCTGCCACTGAGCCGGGTGAAATCCTACCTATGCCCTATGTCAGTGGCCACCCGAGTGC  
AGCTGGTGTGCCACTCTGGTGGCTGAAGCTGCTGCAGCCCCGGCTTCCCTGAGGCGTTGCAGCCAATGTCC  
TGGAGCCACGAGAACATGCTACCCCTGTTGCTACGGGCCACGAGAACGGTGGCCGTGGAGCTCCAG  
ACCCATTCTGGGGTGAAGGCTGCAGCAGCGAGTTAGAGCGACGGTACCCCTGGGACGAGGCTGGCTGGCTCG  
CTGTGCAAGCAGGCCCCCTCCCAGGTGCGACTCATGGACGTGGCTCGAAGAAGCACCCTGAGGACACTCTCT  
TCTTCTTCTACACCGTGTGGACAAGGCTGGCCAGTCTCAACCGCTGTCGATGAATGCCATCTGGCT  
GGCAGGCCCTTCTCCAGTCATTTCCAGGAGTTCAATCTGCCCTGTCACCAACAGAGATCACCCCCAGGGCCCC  
CGGGGGCTGGCCCTGACCCCCCTCCCTGGCTGACCCCTCCGGGGGCTCTATAGGGGGAGATTG  
ACCGGCAGGCTCTGCCGGAGGCTGTTCTACAACGCTGACTACCTGGCGGGCCAGGCCGGCTGGCAGGTGAAC  
TGGCAGGCCAGGAAGAGGAGGAAGGCCCTGGAGGGGCTGGAGGGTATGGATGTTTCTCCGGTTCTCAGGGCTCC  
ACCTCTTCTGGCCGTAGAGCCAGGGCTGGTGAGAACAGTTCTCCCTGCGAGACTGCAGCCCACGGCTCAGTGAAG  
AACTCTACCAACCGCTGCCCTCAGCAACCTGGAGGGCTAGGGGGCGTGCCAGCTGGCTATGGCTCTTTG  
AGCAGGAGCAGGCCAATAGCACTTAGCCCGCCTGGGGCCCTAACCTCATTACCTTCTGTCTGCCAGCC  
CCAGGAAGGGCAAGGCAAGATGGTGGACAGATAGAGAATTGTTGCTGATTTTAAATATGAAAATGTTATTAA  
ACATGTCTCTGCC

## **FIGURE 118**

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPDSRARLD  
QSDEDFKPRIVPYYRDPNPKVLRTRYIQTTELGSRERLLVAVLTSRATLSTLAVAVNRTV  
AHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSETLRHLHTHFGADYDWFFIMQDDTY  
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRG  
DILSARPDEWLGRCLIDS LGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE  
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPEGEAGLSPVGLPAPFTPNSRFEV  
LGWDYFTEQHTFSCADGAPKCPLQGASRADVGALETALEQLNRRYQPRLRFQKQRLLNGYR  
RFDPARGMEYTLDLLECVTQRGHRRRALARRVSLLRPLSRVEILPMPYVTEATRVQLVLPLL  
VAEAAAAPAFLEAFAAANVLEPREHALLTLLVYGPREGGRGAPDPFLGVKAAAELERRYPG  
TRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTTVWTRPGPEVLRCRMNAISGWQAFFP  
VHFQEFPALSPQRSPPGPPGAGPDPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA  
RARLAGELAGQEEEALEGLEVMDFVLFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR  
CRLSNLEGLGGRQLAMALFEQEQQANST

**Signal sequence:**

amino acids 1-15

**Transmembrane domain:**

amino acids 489-507

**N-glycosylation site.**

amino acids 121-125, 342-346

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

**Casein kinase II phosphorylation site.**

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

**Tyrosine kinase phosphorylation site.**

amino acids 736-743

**N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-678

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**Cell attachment sequence.**

amino acids 247-250

## **FIGURE 119**

CGGAGTGGTGCACGTGAGAGGAACCGTGCACGGCTGCCTTCCTGTCCCCAAGCC  
GTTCTAGACGCCGGAAAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTATGCTTGG  
AAGCATTCTGTGCTTGATCACTATGCTAGGACACATTAGGATTGGTCATGAAATAGAA  
TGCACCACCATGAGCATCATCACCTACAAGCTCTAACAAAGAAGATATCTGAAAATTCA  
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTCGAGTATACTGTATTATCCTGTAAAACC  
CAAAGATGTGAGTCTTGGGCTGCAGTAAAGGAGACTGGACCAAACACTGTGACAAAGCAG  
AGTTCTCAGTTCTGAAAATGTTAAAGTGTGAGTCATTAATATGGACACAAATGACATG  
TGGTTAATGATGAGAAAAGCTTACAAATACGCCCTTGATAAGTATAGAGACCAATACAAC  
GTTCTCCTGCACGCCCACTACGTTGCTATCATTGAAAACCTAAAGTATTTTGTAA  
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT  
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTCT  
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTGGAAGATATCTGAAGATAAAC  
AGCTAGCAGTTGCCTGAAATATGCTGGAGTATTGCAAGAAAATGCAGAAGATGCTGATGGA  
AAAGATGTATTTAATACCAAATCTGTTGGCTTCTATTAAAGAGGCAATGACTTACACCC  
CAACCAGGTAGTAGAAGGCTGTTAGATATGGCTGTTACTTTAATGGACTGACTCCAA  
ATCAGATGCATGTGATGTATGGGTATACCGCCTTAGGGCATTGGCATATTTCAAT  
GATGCATTGGTTTCTTACCTCAAATGGTCTGACAATGACTGAGAAGTGGTAGAAAAGCG  
TGAATATGATCTTGTATAGGACGTGTGTCATTATTGTAGTAGTAACATACATATCCAA  
TACAGCTGTATGTTCTTTCTTAATTTGGTGGCACTGGTATAACCACACATTAAAG  
TCAGTAGTACATTTAAATGAGGGTGGTTTTCTTAAACACATGAACATTGAAATG  
TGTTGGAAAGAAGTGTGTTAAGAATAATAATTGCAAATAACTATTAAATAATTAT  
GTGATAAATTCTAAATTATGAACATTAGAAATCTGTGGGGCACATATTTGCTGATTGGTT  
AAAAAAATTAAACAGGTCTTAGCGTTCTAACAGATATGCAAATGATATCTCTAGTTGTGAATT  
TGTGATTAAAGTAAAACCTTGTGTTCCCTTACTTCTAACACTGATTATGTTCT  
AAGCCTCCCCAAGTCCAATGGATTGCCTCTCAAATGTACAACTAAGCAACTAAAGAAA  
ATTAAAGTGAAGTGTAAAAAT

## **FIGURE 120**

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME  
LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAFFSSENVKFESINMDTNMDWLMMRK  
AYKYAFDKYRDQYNWFFLARPTTFAIENLKYFLLKKDPSQPFYLGHTIKSGDLEYVGMEGG  
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT  
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL  
PPNGSDND

**Signal sequence:**

amino acids 1-33

**N-glycosylation site.**

amino acids 121-125, 342-346

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

**Casein kinase II phosphorylation site.**

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

**Tyrosine kinase phosphorylation site.**

amino acids 736-743

**N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-672

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**Cell attachment sequence.**

amino acids 247-250

## **FIGURE 121**

## **FIGURE 122**

MNSSKSSETQCTERGCSSQMFLWTAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN  
FTELCYNYGSGSVKNCCPLNWEYFQSSCYFFSTDTISWALSLKNCSAMGAHLVVINSQEEQ  
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPPNNIATLEDCATMRDSS  
NPRQNWNDVTCFLNYFRICEMVGINPLNKGS

**Signal sequence:**

amino acids 1-42

**N-glycosylation site.**

amino acids 2-6, 62-66, 107-111

**Casein kinase II phosphorylation site.**

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

**N-myristoylation site.**

amino acids 15-21, 74-80, 155-161

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 27-38

## **FIGURE 123**

GGGACTACAAGCCGCCCGCCTGCCGCTGGCCCCCTCAGCAACCTCGACATGGCGCTGAGGCGGCCACCGCGAC  
TCCGGCTCGCGCTCGGCTGACTTCTTCCTGCTGCTGCTTTCAAGGGGCTGCTGATAAGGGCTGAAATC  
TCAAATCCAGCAATCGAACCCCAGTGGTACAGGAATTGAAAGTGTGAACTGTCTGCATCATTACGGATTGCG  
AGACAAGTGACCCAGGATCGAGTGGAAAGAAAATTCAAGATGAACAAACCACATATGTGTTTGACAACAAAA  
TTCAGGGAGACTTGGCGGGTCTGAGGAAATACTGGGAAGACATCCCTGAAGATCTGAATGTGACACGGAGAG  
ACTCAGCCCTTATCGCTGTGAGGTCGTTGCTGAAATGACCGAAGGAAATTGATGAGATTGTGATCGAGTTAA  
CTGTGCAAGTGAAGCCAGTGCACCCCTGCTGTAGAGTGCCGAAGGCTGTACCAAGTAGGCAAGATGGCAACACTGC  
ACTGCCAGGAGACTGAGGGCACCCCCGGCCTCACTACAGCTGGTATCGCAATGATGTACCAACTGCCACGGATT  
CCAGAGCCAATCCCAGATTTCGCAATTCTCTTCACTTAAACTCTGAAACAGGCACTTGTGTTCACTGCTG  
TTCACAAGGACGACTCTGGGAGACTACTGCAATTGCGGAATTATGGGGGGGTTCTGGTGTCTGTACTGCCCTGA  
AGATGGAAGTCTATGACCTGAAACATTGGCGGAATTATGGGGGGGTTCTGGTGTCTGTACTGCCCTGA  
TCACGGTGGGATCTGCTGTGCAACAGCTGAACTTCAACAATAACAGGATGGAGAAAGTTACAAGA  
ACCCAGGGAAACCAAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGCACTTCAGACACAAGTCATCGTTG  
TGATCTGAGACCCCGGGTGTGGCTGAGAGCGCACAGAGCGCACAGTGCACATACACCTCTGCTAGAAACTCCTGCAA  
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTCAGAAAGCTTTCTGTTTGGCAAAGTTGACCA  
CTACTCTTACTCTAACAGCCACATGAATAGAAGAATTTCCTCAAGATGGACCCGGTAATATAACCAAA  
GGAAGCGAAACTGGGTGCGTTACTGAGTTGGGTTCTTAATCTGTTCTGGCCTGATTCCGCATGAGTATTAGG  
GTGATCTAAAGAGTTGCTCACTGAAACGCCGTGCTGGGGCTGTGAAGCCAGCATGTTCAACACTGGTCGTT  
CAGCAGCCACGACAGCACCATGTGAGATGGCGAGGGTGGCTGGACAGCACCAGCAGCGCATCCGGGGAAACCCA  
GAAAAGGCTTCTTACACAGCAGCCTACTTCATCGGCCACAGACACCCACCGCAGTTCTTAAAGGCTCTG  
TGATCGGTGTTGCACTGTCATTGTGGAGAAGCTTTGGATCAGCATTTGTAAGAACACAAAATCAGGAAG  
GTAATTGGTGTGGAAGAGGGATCTGGCTGAGGAACCCGCTGCTTGTCAAACAGGGTGTCAAGGATTAAGGAAA  
ACCTTCGTCCTAGGCTAACTGAAATGGTACTGAAATATGCTTTCTATGGGTCTGTTATTAAAGGAA  
TACATCTAAATTGGCTAAAGGATGTATTGATTATTGAAAGAAATTCTATTAAACTGTAATATATTGT  
CATACAATGTTAAATAACCTATTGTTAAAAAGGTTCAACTTAAGGTTAGAAGTCCAAGCTACTAGTGTAAAT  
TGGAAATATCAATAATTAAAGAGTATTGTTACCAAGGAATCCTCTCATGGAAGTTACTGTGATGTTCTTTCT  
CACACAAGTTTAGCCTTTTCACAAGGAACCTACACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT  
TAAAATTCCAGTTAAAGCAATGTTGAAATCAGTTGCTCTTCAAAGAAACCTCTCAGGTTAGCTTGAAC  
GCCTCTCCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGGCCCTCAGATGTACACACAGATG  
CCAGTCAGCTCTGGGGTGCAGGCCAGGCCACCCGCTCTAGCTCAGTTGCTCTGCTGCTGCCAGGAGGCCCT  
GCCATCCTGGGGCTGGCAGTGGCTGTGCTCCAGTGGCTTACTCAGTGGCCCTTGCTCATCCAGCACAGC  
TCTCAGGGGGCAGTCAGGGACACTGGTCTTCCATGTAGCGTCCAGCTTGGCTCTGTAACAGACCTCT  
TTTGTTATGGATGGCTCAAAAATAGGGCCCCAATGCTATTGTTTTAAGTTGTTAAATTGGTT  
AAGATTGCTAAGGCCAAGGAATTGCAAATCAAGTCTGTCAGTACAATAACATTGTTAAAAGAAAATGGAT  
CCCACTGTTCTCTTGCACAGAGAAAGCACCCAGCAGGCCACAGGCTCTGCGCATTCAAAACAAACCATGAT  
GGAGTGGCGGCCAGTCCAGCCTTTAAAGAACGTCAGGTGGAGCAGCAGGTGAAAGGCTGGGGAGGAAAG  
TGAAACGCCCTGAATCAAAGCAGTTCTAATTGACTTTAAATTTCATCCGGGAGACACTGCTCCATT  
TGTGGGGGACATTAGCAACATCACTCAGAACGCTGTGTTCTCAAGAGCAGGTGTTCTAGCCTCACATGCCCT  
GCCGTGCTGGACTCAGGACTGAAGTGTGTAAGCAAGGAGCTGCTGAGAAGGACACTCCACTGTGTGCCCTGGA  
GAATGGCTCTCACTACTCACCTGTCTTCAGCTCCAGTGTCTTGGGTTTTTAACTTTGACAGCTTTTTT  
AATTGCATACATGAGACTGTGTTGACTTTTTAGTTATGTGAAACACTTGCCGAGGCCCTGGCAGAGGCA  
GGAAATGCTCCAGCAGTGGCTAGTGTCCCTGGTGTCTGCATGGCATCCTGGATGCTTAGCATGCAAGTTC  
CCTCCATCATTGCCACCTTGGTAGAGAGGGATGGCTCCACCCCTCAGCGTTGGGATTACGCTCCAGCCTCCT  
TCTTGGTTGTCTAGTGTAGGGTAGCCTTATTGCCCTCTTCTTAACTCCCTAAACCTCTACACTAGTGCCTA  
TGGGAACCAGGTCTGAAAAGTAGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGCTGCTATAACTGAGACTAGA  
CGGAAAAGGAATACTCGTGTTAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT  
GCCCTTGGATGGATGGTGTGACACAGATGCTACAGACTTGTACTAACACACCGTAATTGGCATTGTTAAC  
CTCATTATAAAAGCTTCAAAAAACCCA

## **FIGURE 124**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLSKIWNVRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTPVCRVPKAVPGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGG
VLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRKSSFVI
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 243-263

**N-glycosylation sites.**

amino acids 104-107, 192-195

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-110

**Casein kinase II phosphorylation site.**

amino acids 106-109, 296-299

**Tyrosine kinase phosphorylation site.**

amino acids 69-77

**N-myristoylation sites.**

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267